STIC-Biotech/ChemLib

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From: Sent: To: Subject:

Davis, Minh-Tam Tuesday, March 11, 2003 3:01 PM STIC-Biotech/ChemLib Search request for 09/847046

Please search in commercial database, PGPUB, and issued patent files:

1) SEQ ID NO:1 and 2.

Thank you. MINH TAM DAVIS

ART UNIT 1642, ROOM 8401, MB 8E12

305-2008

Oct 2000 purity date

Edward Hart

Technicai Info. Specialist

STIC/Biotech

CMI 6B02 Tel: 305-9203

Searcher:

Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:

NA Sequences:

AA Sequences:

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
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Human immune syste	Human musculoskele	Human GABA transpo	Human secreted pro	Genomic DNA encodi	_	-	Human immune/haema	Human cDNA differe	Human transporter	Human bone marrow	Human brain expres	Human foetal liver		Human immune syste	Genomic sequence o		Human cervical can	Genomic DNA encodi		Human reproductive	Human cDNA differe	Human nervous syst	Serglycin - proteo		Human immune/haema			Human immune/haema	_			encoding s		prostate	Human secreted pro

ALIGNMENTS

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13-OCT-2000;

08-DEC-2000;

08-DEC-2000;

24-JAN-2001;

16-MAR-2001;

16-MAR-2001;

06-APR-2001;

24-APR-2001;

30-APR-2001;

04-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                       Prostate cancer; prostate tumour tissue; human; mammal; cytostatic; gene therapy; gene; ds.
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2000US-0687576.
2000US-0733288.
2000US-0733742.
2001US-263957P.
2001US-276791P.
2001US-2767888P.
2001US-281922P.
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ABR92115 ABR92263 represent prostate cancer associated polynucleotide concernes.
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760	l CTCTGAGAATAAAGCATTGGAATAGAAGTAATTGGTTTAAAGAAGCAGAAAAATCATTTA 27	2701	Qy
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580 580	TACCTGCTCAAGAATGGAAACCTCCTCTTCCAGCTTATGATTTTCTAAGTATGATAGATG 2: 	2521 2521	Фр
520 520	AAAACCTTGTATTGTGGCTGAAGAAATTAGAAGCAGGACTAGAAAATCATATCACAATTT 2	2461 2461	Db Qy
460 460	TGAATCTGCATTCAGGTGGCCAAGTATTTGCATTTCCTTCAGACCAGGCTATAATTGAAG 2. 	2401	D Q
400	GGAGAGGAATCTTGCGGGCATATTTTGATCCTCTGCCTCCCCTTCCTT	2341 2341	Qy Db
340 340	L AGCAGAAATACTTGGATTCATTTACTCCATGCTGGTTAAATCTAAAGAATACTCCAGTGG 2: 	2281 2281	Db Qy
280 280	TTTTGTTCAGTGATGGCACTGTAAATCCTCAATATAAAAAAGCAATATTGACACTGGTAA 2	2221 2221	Db Qy
220 220	TTCCGGAAATCACTGTGGAAAATCTTCCCAGTTATTTCAGACTTCAGAAACCATTATTGA 2: 	2161 2161	рь
160 160	L TAGCTAGCACACATGCACAAGACATAGTTCAAATAACAGATGCACAGACTGGAAATGT 2: 	2101 2101	dq VQ
100	CAAGTCTTCCAGCCCTGCTGCCTGCCAGACACACAGAAGGCAAAATAGAGAGCATCCCAC 2	2041	D 64
040	ATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACTGTCAACCAAATATGCTG 2	1981 1981	dd Qy
980 980	GTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAGGAAACTACCTAAAAGGAT 1 	1921 1921	Db Qy
920 920	GTGGGGAATTATATAAAGACCTCATCTTGTATTCTAGTGTGTCAGTATTGGGACTATTTA 1	1861 1861	DP 6A
860	TCAACAGGATTTCATATCCAGTGAATATAACATCGATCCAAGAAGCAGAAGAATATTTAA 1	1801 1801	D Qy
800	AGAACCCAGTATCTTATGCTGGAATGTTAGGAACCAAAGATCTCCTAAAATTTATCCAGC 1	1741 1741	Фр
740	1 ATGTATGTACTAAGCAAAATGTTACTGAATTTCCTATCATAAAGATGTACAAGAAAGGCG 1	1681 1681	Qу
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AATTTCAGATTGAACAGGGATTCAGCATTCTGCCATCTCCTCATGGAAAGAGAGGGGTCCC 3	TTATATTTTAAGTGAGTCTTAAAACCCTCCTCATTTCTACAAGTTATATGGCT	ATTTATATTTTAAGTGAGTCTTAAAACCTCCTCTTATTTCTACAAGTTATATGGCTA 3	CTTGATCTTTTCTAATATTTTCAGAAAGTGATGGGATAACCCTAGAAGAGGACTCAGAAT 3 	AATTTTGGCTATTAAAGATATGTATTAGATGGTCTTATCCTGATTATTACCTGGATACAA 3	ACCTGTGGCAGACTAGGTTTCCAGAATTTCCTGGTTCTGCTCACGTATCATGTTTGAAAA 3	AGAATTATCCTGCCCGAAATGGTAGTCGTGCCAAGGCTGAGTAACCTTGTGTTAAAAGTA [GTGAGTAGAGGCCATGGATCCTGCTAAATAACCTGCATTGGACAGGCCCCCCACAACAA 	GATATTTAGCAATTGTCGGGAGACATTTTTGATGTCATGACTAGGGCAGTTATTGACATT 3	ACACTTATATTTGTTTATTGGAGTCATGATATTAAAATCAGCGTTTGTCAACCTCAGGG 3	ATTTGGATTAAAATTAAACTCTAATCACAGTTAACTCCACAGTGCATTCATGCAGC 	ATTGGACAGTTCAGTACTAGACAAAACTAGCATAATTAACTTAGTTCTAGCCATGATTT 3	CTTACTTCCGAGTAGCCATATTTCAAGTGTTCATTGCCACATGTGGCCTGTGACTACTGT 3	TACATCCTTTTTTGTACCAAGTCTTCTAAATGCAGTACATATTTTATACTTACT	ACTTTTCACCCAGTAGTATACCCAAAATAGCGAAATATAGAAATTATTAATGAGATATTT 3 	ATTTTCTAGTAACTACATTAAACAAAGTAAAAGTGAGCAGGGCAAAATAATTTTGATATT 3	AAGTTTGCAGACTAGTGCCATCCAATAGAATTATAATATAAGTCACATATTTTATTTA	AAATTTTTTTGGCATGATAGACTTAATTTATTTCCTTAAAGAATAATATTAAATCATTTC 2	GACGTGATAAAGAGTTAGGATGCTCAAAAGTGAACTAATTTATAGGGCTGTGGTTTCCA 2 	
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                                                                                                                                                                                                                               primer;
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The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to a combination of a polynucleotide which comprises a 5'-end cc polynucleotide which comprises a 1'-end cc polynucleotide comprises a 3'-end sequence complementary to a combination of the 5'-end sequence. The primer sets can be used in antisense therapy and cc particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, comprises are useful for synthesising polynucleotides. Cc particularly full-length cDNAs. The primers are also useful for the code detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and CAAH3633 to AAH18742 represent human cald sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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02-MAY-2000; 3
09-JUN-2000; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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Otsuki
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Sequence 2820 BP; 911 A; 496 C; 504 ç; 909 T; 0 other;

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Query Match

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               ATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACTGTCAACCAAATATGCTGCAAGT
                                              ACCATGAAAACAGCAAAAGAAGTTTTAGTGAAGCAGGAAACTACCTAAAAGGATATGTT
                                                                              CTTCCAGCCCTGCTTGCCAGACACACAGAAGGCAAAATAGAGAGCATCCCACTAGCT
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nilarity 99.8%;
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,	3185 1500	TTCCGAGTAGCCATATTTCAAGTGTTCATTGCCACATGTGGCCTGTGACTGAC	3126 1441	Qy
	3125 1440	CCTTTTTTGTACCAAGTCTTCTAAATGCAGTACATATTTTATACTTACT	3066 1381	Ωy
	3065 1380	TCACCCAGTAGTATACCCAAAATAGCGAAATATAGAAATTATTAATGAGATATTTTACAT 	3006 1321	Оу
	3005 1320	CTAGTAACTACATTAAACAAAGTAAAAGTGAGGAGGGCAAAATAATTTTGATATTACTTT	2946 1261	Оу
	2945 1260	TGCAGACTAGTGCCAÌCCAATAGAATTATAATATAAGTCACATATTTTATTT	2886 1201	ДУ
	2885 1200	TTTTTGGCATGATAGACTTAATTTATTTCCTTAAAGAATAATATTAAATCATTTCAAGTT 	2826 1141	Оу
	2825 1140	GATAAAGAGTTAGGATGCTCAAAAGTGAACTAATTTTATAGGGCTGTGGTTTCCAAAATT	2766 1081	Qy Db
	2765 1080	AGAATAAAGCATTGGAATAGAAGTAATTGGTTTAAAGAAGCAGAAAAATCATTTAGACGT	2706 1021	Qу
:	2705 1020	AATGATAAGGAACAACATGAAGATAAATCGGCAGTCAGAAAAGAACCGATTGAAACTCTG	2646 961	Оу
	2645 960	ACATCTCAACGTGGCACTAGGANAGTTCCCAAGTGTATGAAAGAAACAGATGTGCAGGAGIIIIIIIIII	2586 901	DP QA
	2585 900	GCTCAAGAATGGAAACCTCCTCTTCCAGCTTATGATTTCTAAGTATGATAGATGCCGCA 	2526 841	Оy
	2525 840	CTTGTATTGTGGCTGAAGAAATTAGAAGCAGGACTAGAAAATCATATCACAATTTTACCT	2466 781	D 64
	2465 780	CTGCATTCAGGTGGCCAAGTATTTGCATTTCCTTCAGACCAGGCTATAATTGAAGAAAAC	2406 721	Db Qy
	2405 720	GGAATCTTGCGGGCATATTTTGATCCTCTGCCTCCCCCTTCCTCTTCTTTTTGGTGAAT	2346 661	Ωу
	2345 660	AAATACTTGGATTCATTTACTCCATGCTGGTTAAATCTAAAGAATACTCCAGTGGGGAGA	2286 601	Qy
	2285 600	TTCAGTGATGGCACTGTAAATCCTCAATATAAAAAAGCAATATTGACACTGGTAAAGCAG	2226 541	Qу
	2225 540	GAAATCACTGTGGAAAATCTTCCCAGTTATTTCAGACTTCAGAAACCATTATTGATTTTG	2166 481	Qy Db
	2165 480	AGCACACATGCACAAGACATAGTTCAAATAACTAACAGATGCACTACTGGAAATGTTTCCG	2106 421	Qу
	420	CTTCCAGCCCTGCTGCCTGCCAGACACACAGAAGGCAAAATAGAGAGCATCCCACTAGCT	361	Db

4265 2580	6 TCCTTATAACATAGACCCGTTGCTACTCTCAGCACCCTCTCCTCAATTTTTTTT	Qy 420 Db 252	п с
4205 2520	6 TGATTTTATAAGTGAAATTTAAGGAATCTAACAGGTAAAACTCAGTAAGTGCATMTATT 	Qy 414 Db 246	п о
4145 2460	6 AATATCTACTTGATATCTTGTTCTTTAAATTTTCTTCACATATGGTTTGCCTGATACAAC)y 408)b 240	п о
4085 2400	6 CATTITITGAGACATITGTIGAGAATATICTATITGGTGCTCTACTGTATITITCTITIT 	Qy 402 Db 234	п о
4025 2340	6 ATCACTTAGCTGTTAGACTGATCTGTTTGTAGCAGTTGTTTGT	Qy 396 Db 228	
3965 2280	6 CACACGGCCTCATTCTGTGAGGGAGGGAAAGATTAGCCAAAGAGTTAATTTTCATTCCAA 	Qy 390 Db 222	
3905 2220	6 TGAAGCGTCTCTGAAATCTACCCTTGCAAGCTTCAGACAAATCAGTTGATCTCCCTGAGC 	Qy 384 Db 216	
3845 2160	6 CAGATTGAACAGGGATTCAGCATTCTGCCATCTCCTCATGGAAAGAGAGGCTCCCTCATC	Qy 378 Db 210	
3785 2100	6 TTATATTTTAAGTGAGTCTTAAAACCTCCTCTTATTTCTACAAGTTATATGGCTAAATTT 	Qy 372 Db 204	;
3725 2040	6 TCTTTTCTAATATTTTCAGAAAGTGATGAGATAACCCTAGAAGAGGACTCAGAATGATAT 	Qy 366 Db 198	
3665 1980	6 TGGCTATTAAAGATATGTATTAGATGGTCTTATCCTGATTATTACCTGGATACAACTTGA 	19	
3605 1920	6 TGGCAGACTAGGTTTCCAGAATTTCCTGGTTCTGCTCACGTATCATGTTTGAAAAATTT	Qy 354 Db 186	
3545 1860	6 TATCCTGCCGAAATGGTAGTCGTGCCAAGGCTGAGTAACCTTGTGTTAAAAGTAACCTG	 ω	T 0
3485 1800	6 AGTAGAGGCCATGGATCCTGCTAAATAACCTGCATTGGACAGCGCCCCCACAACAAAGAAT	Qy 342 Db 174	
3425 1740	6 TTAGCAATTGTCGGGAGACATTTTTGATGTCATGACTAGGGCAGTTATTGACATTTAGTG	Qy 336 Db 168	п О
3365 1680	6 TATATTTGTTTTATTGGAGTCATGATATTAAAATCAGCGTTTGTCAACCTCAGGGGATAT 	Qy 330 Db 162	
3305 1620	6 TGGATTAAAATTAAACTCTAATCACAGTTAACTCCACAGTGCATTCATGCAGCTGACAGT 	Qy 324 Db 156	
32 4 5 1560	6 ACAGTTCAGTACTAGACAAAAACTAGCATAATTAACTTAGTTCTAGCCATGATTTCTATT	Qy 318 Db 150	מט

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                   cancer in a patient (d) assessing the a in a patient; (e) selecting a com (f) assessing the patient; (d) assessing the a patient; (e) is also useful
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13-DEC-2000;
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25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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                                                                  selecting a composition for inhibiting prostate cancer is assessing the prostate cell carcinogenic potential of a determining whether prostate cancer has metastasized in assessing the aggressiveness or indolence of prostate ca
                                                                                                                                                                                                                                                                                                                                                                                                            detecting
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GAAAGAAACAGATGTGCAGGAGAATGATAAGGAACAACATGAAGATAAATCGGCAGTCAG
                                              TCTAAGTATGATAGATGCCGCAACATCTCAACGTGGCACTAGGAAAGTTCCCCAAGTGTAT
                                                                        AAATCATATCACAATTITACCTGCTCAAGAATGGAAACCTCCTCTTCCAGCTTATGATTT
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for detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             el isolated nucleic acid molecule associated with cancerous state of state cells and correlating with presence of prostate cancer, useful detecting presence of prostate cancer -
TCAGAAACCATTATTGATTTTGTTCAGTGATGGCACTGTAAATCCTCAATATAAAAAAAGC
                                                                                                   AATAGAGAGCATCCCACTAGCTAGCACACATGCACAAGACATAGTTCAAATAATAACAGA
                                                                                                                                                                                                   AAACTACCTAAAAGGATATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACT
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                                                  TCAGAAACCATTATTGATTTTGTTCAGTGATGGCACTGTAAATCCTCAGTATAAAAAGC
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97.3%;
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344 GTTTGTCAACCTCAGGGG
3284 GTGCATTCATGCAGCTGACAGTTATATTTO
3224 AGTTCTAGCCATGATTTCTATTTGGATTAAAATTAAACTCTAATCACAGTT
3164 TGGCCTGTGACTACTGTATTGGACAGTTCAGTACTAGACAAAAACTAGCATAATTAACT
3104 TTATACTTACTGCATTTCTTACTTCGAGTAGCCATATTTCAAGTGTTCATTGCCAC
3044 TTATTAATGAGATATTTTACATCCTTTTTTGTACCAAGTCTTCT
290 MARKIMIIIIGA IA II KOLIIIIKKO KOKO KASIASIKO KOKO KASIASIKO GARAIA (H. 1888).
924 CACATATTTTATTT
2864 TAATATTAAATCATTTCAAGT
2804 TAGGGCTGTGGTTTCCAAAATTTTTTTGGC
2744 AGCAGAAAAATCATTTAGAC
2684 AAAAGAACCGATTGAAACTC'
2624 GAAAGAACAGATGTGCAGGAGAATG
2564 TCTAAGTATGATAGATGCCGCAACATCTC [
2504 AAATCATATCACAATTTTACCTGCTCAAG
2444 CCAGGCTATAATTGAAGAAAACCTT
2384 TCCTCTTCTTGTTTTGGTGAATCTGCATTCAGGTGGCCAAGTATTTGCATTTCCTTC.
2324 AAAGAATACTCCAGTGGGGAGAAGGAATCTTGCGGGCATATTTTGATCCTCTGCCTC

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RESULT 5
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                                                                                                  TATTTCTAATATGGGAACAATGAGAGTGAACTCTAAATATAGGTTGTAGTAATAAAACAT
                                                                                                                                                              AAACTCAGTAAGTGCATMTATTTCCTTATAACATAGACCCGTTGCTACTCTCAGCACCCT
                                                                                                                                                                                                                                                                                                                                   TGGAAAGAGAGAGCTCCCTCATCTGAAGCGTCTCTGAAATCTACCCTTGCAAGCTTCAGAC
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        entry)
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AGGATTTCATATCCAGTGAATATAAACATCGATCCAAGAAGCAGAAGAATATTTAAGTGGG CCAGTATCTTATGCTGGAATGTTAGGAACCGAAGATCTCCTAAAATTTATCCAGCTCAAC

1865

120

TGTACTAAGCAAAATGTTACTGAATTTCCTATCATAAAGATGTACAAGAAAGGCGAGAAC

TGTACTAAGCAAAATGTTACTGAATTTCCTATCATAAAGATGTACAAGAAAGGCGAGAAC

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1686

Query Match Best Local Similarity Matches 778; Conserv

Conservative

0;

Score 776.2; DB 22; Pred. No. 2.9e-170; 0; Mismatches 6;

Indels Length

Gaps

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784; 0;

17.1%; A; 149

Sequence

784

ВP;

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148

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222 T;

3 other;

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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the CC collyonucleotide comprises at least 15 nucleotide specification, where the CC ollyonucleotide comprises as sequence complementary to the CC of an oligonucleotide comprising a sequence complementary to a complementary full sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length CC AAH13633 to AAH18742 represent human cold sequences; and AAH13628 and CC AAH13633 to AAH18742 represent human cold sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesi full-length cDNAs define and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ
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, Sugiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                         2158;
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T, Wakamatsu
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A, Naga
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Otsuki
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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                 2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                   2001WO-US05171
                                                                                                                                                                                                                                                                                                                                  cancer;
marker;
                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                  gene;
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                                                                                                                                                                                                                                                                                                                                                        carcinogen;
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pharmacogenomic

prostate

marker;

gene; cytostatic;

carcinogen;

pharmacodyanamic marker;

3034

Human 13-SEP-2002 ABV03043;

prostate expression marker cDNA

(first

entry)

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RESULT 7
ABV03043
ID ABV0
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AC ABV0
XX
DT 13-S
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DE Huma
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KW Huma
KW Phar
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OS Homo
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(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
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(I) is a
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                                                                                                                                                                                                                                                                                                                     GTATTGGGACTATTTAGTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAGGA
                                                                                                                                                                                                                                                                                                                                                          AACTACCTAAAAAGGATATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also
                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                           ВP
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Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INC
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Best Local S
Matches 350
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                          (a) assessing v
(b) monitoring
(c) assessing 1
cancer in a partient;
(d) assessing 1
in a patient;
(e) selecting 2
(f) assessing 1
(g) determining
(h) assessing 1
patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                 1905
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                                                                     1965
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                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                            AACTACCTAAAAGGATATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACTG
                                                                                                      GTATTGGGACTATTTAGTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAGGA
                                                                                                                                                GCAGAAGAATATTTAAGTGGGGAATTATATAAAGACCTCATCTTGTATTCTAGTGTGTCA
              GTATTGGGACTATTTAGTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAGGA
                                                                                                                                     GCAGAAGAATATTTAAGTGGGGAATTATATAAAGACCTCATCTTGTATTCTAGTGTGTCA
                                              AACTACCTAAAAGGATATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACTG
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                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                            useful as
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2000US-211314P.
2000US-219007P.
2000US-255281P.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                       therapy
                                                                                                                                                                                                                                                                      348.8; L.
No. 4.3e-71;
                                                                                                                                                                                                                                                                                                                       95
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                                                                                                                                                                                                                                                                                                                                                                                                                       for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                          pharmacogenomic marker
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RESULT 8
ABV33357
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XX ABV3
XX ABV3
XX ABV3
XX Huma
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Best Local
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(d) assessing the efficacy of a therapy ror ......
(in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                          1725
                                                                                                                                      1785
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                                            1845
                                                                                                                                                                                                                                                                                                                                                            Sequence 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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18-JUL-2000;
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25-MAY-2000;
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  166
                                                                                         106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assessing whether a patient is afflicted with prostate cancer; monitoring the progression of prostate cancer in a patient; assessing the efficacy of a test compound to inhibit prostate
ATGTACAAGAAAGGCGAGAACCCAGTATCTTATGCTGGAATGTTAGGAACCAAAGATCTC
                                                                                                                                      CTAAAATTTATCCAGCTCAACAGGATTTCATATCCAGTGAATATAACATCGATCCAAGAA
                                                                                                                                                                                  AGGTACAAGAAAGGCGAGAACCCAGTATCTTATGCTGGAATGTTAGGAACCGAAGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,,</u>
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gene; ss.
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                                                                                                                                                                                                                                                                e 348.8; Du No. 4.4e-71;
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                                                                                                                                                                                                                                                                                                                                                                Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eic acid molecule (I) comprising (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                0 other;
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test cancer in a patient;
                                 in a pat
(e) sele
(f) asse
(g) dete
(h) asse
patient;
                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2025
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  Sequence
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                                                                                                     cancer in a patient;(d) assessing the efficacy of a therapy for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001WO-US05171
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                                                                                            a patient;
                                            selecting a composition for i
assessing the prostate cell o
determining whether prostate
assessing the aggressiveness
                        is also
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                       useful as a
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marker; gene; ss.
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  88
                                            carcinogenic potential of a e cancer has metastasized in s or indolence of prostate ca
                                                                              inhibiting prostate cancer in a patient;
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                       or pharmacogenomic
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Query Match

348.8;

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         The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from ollating-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included.
CDNA
5' ES
                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1965
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                                                                                                                                                   Claim
                                                                                                                                                                            diagnostic,
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ESTs are derived
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                                                                                                                                                  SEQ ID 32911; 71pp + CD-ROM; English.
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                                                                                                                                                                            forensic,
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mRNAs with
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                                                                                                                                                                                                                                                           Giordano
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer
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                                                                                                                                                             (MILL-)
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les 349; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 341; DB 21; Pred. No. 2.7e-69;
                                                                                                                                                           MEDICINE
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RESULT 12
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Best Local :
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                             Homo
                                                                                                                                                                                                                                                                                           4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer in a patient;
(d) assessing the efficacy of a therapy for in a patient;
(e) selecting a composition for inhibiting partial of the prostate cell carcinogenic contents.
                                                                                                                 Human; prostate pharmacogenomic
                                                                        WO200160860-A2
                                                                                                                                                 Human
                                                                                                                                                                                            ABV25366;
                                                                                                                                                                                                                ABV25366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTACTTGATATCTTGTTCTTAAATTTTCTTCACATATGGTTTGCCTGATACAACTGAT 4149
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marker; gene; ss.
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98.1%;
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17-FEB-2000; 16-MAR-2000;

2000US-183319P 2000US-189862P 2001WO-US05171

20-FEB-2001; 23-AUG-200:

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RESULT 13
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ID AAF93
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AC AAF93
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Best Local S
Matches 317
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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
  AAF93519;
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(a) assessing whether a patient is afflicted with prostate cancer:
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                 AAF93519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Pred. No. 9.
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Best Local Sin
Matches 348;
                                                                                                                                                                                                                                                                                                                                                  Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various different human tissue cDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT polypeptide, and an antibody which binds to SRT. The polynucleotide sequence can be used in gene therapy and is useful in the recombinant production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, to map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polynucleotide sequences can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA section.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a SRT polypeptide for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy -
                                                                                                                                                                                                                                                                                                               Sequence 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1999;
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                      351
                                                                                                      229
                                                                                                                                                         173
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                                                                                                                                                                                                             114
                                                                                                                                                                                                                                     111
                                                    289
                                                                            291
CCCCGCCCGCAGGTCCCGGGCAGATAACATAGATCATCAGTAGAAAACTTCTTGAAGTTG
                                                    -- CAGCATGAAGTGTTGTCTTAGGAAACAGAACAGAGTGAAAAAAACAGACAAAATCC
                                                               ACAGCATGGAAGTGTTGTCTTAGGAAACAGAACAGCAGCAGTGAAAAAAACAGACAAAATCC
                                                                                                                                                         CCCGGCCGCAAGGTCCGGGCCAATACATAGTCATCAGTAG----
                                                                                                                                                                                                             CCTCCTCCTCCGTGGGTGCGGCGGGAATNTTGGCCGGNCGGCCTTGGG-ACGGCCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Fig 340; 663pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRT;
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                  BP.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRT protein isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0145701
                                                                                                                                                                                                                                                                                                                  155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                        6.4%;
                                                                                                                                                                                                                                                                                                                 A; 117 C; 131 G; 139 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                           Score 290; DB 22;
Pred. No. 2.3e-57;
                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human retina tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           typing;
                                                                                                                                                         - AAACTTCTTGAAGTTG
                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                        547;
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                         410
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RESULT 14
ABV08367
ID ABV08
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XX Human
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XX 20-FE
PR 11-FE
PR 11-JE
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                                                                                                                                    Query Match
Best Local S
Matches 301
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
  4149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             (d) assessing
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV08367
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                                               43
                                                                                                                                                                                                                                                                                                                   selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                           is
                                        CCTCAGAAATATTTTAGTACATTGCAACCAGG
TTTTTATAACTGAAATTTAAGGAATCTAACAGCTAAAACTCAGTAAGTGCATMTATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                                                                           also
                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                         useful as a pharmacodyanamic or pharmacogenomic
                                                                                                                                                                                                                                B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                the efficacy of a therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression marker cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marker; gene;
                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA;
                                                                                                                                                       5.2%;
92.6%;
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                                                                                                                                                                                                                              Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; carcinogen;
                                                                                                                                                                                                                                86 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monahan
                                                                                                                                      1;
                                                                                                                                                         Score 234.6;
Pred. No. 1.0
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                                                                                                                                                                                                                              75 G; 168 T;
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8358
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                                                                                                                                                            1.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                for inhibiting
                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                            2 other;
                                                                                                                                      15;
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                                                                                                                                      Indels
                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate
                                                                                                                                                                                   447;
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                                                                                                                                                                                                                                                                           marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising of the
                                                                                                                                    Gaps
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RESULT 15
AAS26179
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                            14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
07-JUN-2000;
                                                                   14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                        24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4322
                                                                                                                                                                                                                                                                                                                                       cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                              Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; carebroprotective; nootro neuroprotective; antibacterial; virucide; fungicide; opthal vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4381
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                                                                                                                    07-JUL-2000;
07-JUL-2000;
                                                                                                                                        28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                 11-JUL-2000;
                                                                                                           11-JUL-2000;
                                                                                                                                                                                                                                         31-JAN-2000;
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                                                                                                                                                                                                                                                                                02-AUG-2001
                                                                                                                                                                                                                                                                                                    WO200155322-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS26179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAATGCTAATTAAGTACCTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
2000US-0179065
2000US-018628
2000US-01886350
2000US-019874
2000US-0199076
2000US-0199076
2000US-0299467
2000US-0214886
2000US-0214886
2000US-0214687
2000US-0216880
2000US-0217487
2000US-0216880
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0218290
2000US-0218290
2000US-0224518
2000US-0225218
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225266
                                                                                                                                                                                                                                                            2001WO-US01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   opthalmalogical;
                                                                                                                                                                                                                                                                                                                                                                                                             nootropic;
                                                                                                                                                                                                                                                                                                                                                                                 cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
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The invention relates to isolated nucleic acid molecules and their cc encoded secreted proteins. The nucleic acids and proteins are used to cc prevent, treat or ameliorate a medical condition in e.g. humans, mice, cc rabbits, goats, horses, cats, dogs, chickens or sheep. They cc are also used in diagnosing a pathological condition or susceptibility ct to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in cc diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. bisorders which are diagnosed or treated cc include autoimmune disorders e.g. rheumatoid arthritis, cyperproliferative disorders e.g. rheumatoid arthritis, cc ardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders cc e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. called ocular disorders e.g. corneal infection, and many other can doubt a disorders e.g. corneal infection, and many other consoluted to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before crease and additive or presentative to increase or decrease alterate strange and in chemotaxis. The polypeptides can also be used to additive or presentative to increase or decrease aforace.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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06-DEC-2000
06-DEC-2000
08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecul
diagnosing, preventing,
used as food additives (
                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
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-PSDB; AAU16192.
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-NOV-2000;
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-NOV-2000;
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                                                                                                                                                                                                                                                                                                                           SEQ
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2000US-0246610.
2000US-0246611.
2000US-0246611.
2000US-0246613.
2000US-0249207.
2000US-0249210.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249213.
2000US-0249216.
2000US-0249216.
2000US-0249216.
2000US-0249216.
2000US-0249216.
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SUMMARIES

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ORGANISM
Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
clone:fj0047651.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:7243068.
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Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa
Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sa
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Direct Submission
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Homo sapiens teratocarcinoma cell_line:NT2
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                                                                                                                          Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-348-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
                                                                                                                                                                                                                                                                                                                                                    Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamotto,J., Isono,Y. Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
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/tissue_type="testis"
/clone_lib="TESTI2"
/note="cloning vector
                                                                                                tation: HRI and RAB.
Location/Qualifiers
                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                           /clone="TESTI2039177"
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                                           TGACCCAGCAATGTAGAAGAACACTAATGGAACAGCCATTGACTACACTGAACATTCACC
                                                                                                 GCTCTGAGGATGTGGAATATGCACATCTCTACTTTTTCATTGTAAACTAGTCTTGGACT
                                                                                                                                                          TGTATGGGACTACATACCAATTTGTCTTAACCACAGAAATTGCCCTTTTGGAAAGTATTG
                                                                                                                                                                      TGTATGGGACTACATATCAATTTGTCTTAACCACAGAAATTGCCCTTTTGGAAAGTATTG
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780 864 720

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600 684 48C 564 42C 504 360

540 624 498

300

378

180 318 120 60

2;

2082 2100	TGTCAACCAAATATGCTGCAAGTCTTCCAGCCCTGCTGCTTGCCAGACACACAC	2023	Qу Db
20	GAAACTACCTAAAAGGATATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTAC	1963 1981	Qу
19 19	CAGTATTGGGACTATTTAGTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAG	1903 1921	D Qy
19 19	AAGCAGAAGAATATTTAAGTGGGGAATTATATAAAGACCTCATCTTGTATTCTAGTGTGT	1843 1861	Оy
184 186	AATTTATCCAGCTCAACAGGATTTCATATCCAGTGAATATAAA 	78	Оу
178 180	TGTACAAGAAAGGCGAGAACCCAGTA: 		Db Qy
172 174	ACTGTGCAGATTGGTCTGATGTATGTACTAAGCAAAATGTTACTGAATTTCCTATCATAA	1681	DP QA
166 168	TCTAGTCCTTAGTTCCTGCCG	1632 1621	Db Qq
162	CTTGTCTGCTCCTTACAGCACACATGGCTGGCAGAGAAGGGAAGACAGAGCG	56	В
163		1632	δÃ
163 156	CATTTTTGCAATCCTATATTGATGTGGGAGTTAAACTGAAA 	1585 1501	р _у
158 150	ATGCAACAGTGATGGCTTCTGACAGCATAGTACTCTTCTATGCTGGTTGGCAAGCAGTAT	1525 1441	Qу
152 144	GAGATAGGAAGAAAATTACCTTTGGAACTTACAGTGGAACTAACAGAAGAACATTTA 	1465 1381	Db Qy
146 138	ATGACATGGAAGGTCCAGATATAGATGTTCAGGATGATGAAGTGGCAGAAACTGTTTTCA	1405 1321	Оy
140 132	TAATAATATCTCATGTGGAAAATAATATGCACATTGAGGAAATACAAGAAGATGAAGACA	1345 1261	gb Qy
13 12	TCTTCAAAAGAGCAGAAGAGGGAGTTCCAGTGGAATTTTTGGTATTACATGATGTTGATT	1285 1201	рb
128 120	GAGTTCTACTCTTGTTAAGGGACTCTTTGGAAGTGAACATTCCTCAAGATGCTAATGTGG	1225 1141	р 9
122 114	CTTATGAAGCTGATAGAAGAACTGCAGAATGGGTTGCTTGGCGTCTTCTGGGAAAAGCAG 	1165 1081	ОУ
116 108	TTTCAACTGTCCATCTCCAACTGGGCTTACCACTGGTTTTATTGTTAGCCAACAGGCTA	1105 1021	Qy Db
10	TGTTTATTAAGACAATGAAAGCACCTCTGTTGACTGAAGTTGCTGAAGATCCTCAACAAG	961	DЬ

JO JO REFE AU	VERSION KEYWORDS SOURCE ORGANIS REFERENCE AUTHORS	RESULT AC02569 LOCUS DEFINIT	Дb	Db	Qy	Db Qy	Qу	Фр	Qy Db	Оy	Qу	ОУ	Qу	Qy Db
JOURNAL JOURNAL REFERENCE AUTHORS	ERSION EYWORDS OURCE ORGANISM ORGANISM EFERENCE AUTHORS	ULT 4 125659/c US INITION	2701	64	2623	2563 2581	2503 2521	2443 2461	2383 2401	2323 2341	2263 2281	2203 2221	2143 2161	2083 2101
Homo Sapiens, Clone RF11-263N1/ L Unpublished E 2 (bases 1 to 161100) E 2 (bases 1 to 161100) Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., S Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Anderson,S., Baldwin,J., Barna,N., Burkett,G., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,	AC025659.3 GI:8705128 HTG; HTGS_PHASE1; HTGS_DRAFT. HOMO Sapiens ! Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 161100) Birren,B., Linton,L., Nusbaum,C. and Lander,E.	AC025659 161100 bp DNA linear HTG 25-JUN-2000 Homo sapiens clone RP11-263N17, WORKING DRAFT SEQUENCE, 15 unordered pieces.	GAAAAGAACCGATTGAAACTCTGAGAATAAAGCATTGGAATAGAAGT 2729 - - - - - - - - - - - -		TGAAAGAAACAGATGTGCAGGAGAATGATAAGGAACAACATGAAGATAAATCGGCAGTCA 2682	TTCTAAGTATGATAGATGCCGCAACATCTCAACGTGGCACTAGGAAAGTTCCCAAGTGTA 2622	AAAATCATATCACAATTTTACCTGCTCAAGAATGGAAACCTCCTCTTCCAGCTTATGATT 2562 	ACCAGGCTATAATTGAAGAAAACCTTGTATTGTGGCTGAAGAAGTTAGAAGCAGGACTAG 2502 	TTCCTCTTCTTGTTTTGGTGAATCTGCATTCAGGTGGCCAAGTATTTGCATTTCCTTCAG 2442 	TAAAGAATACTCCAGTGGGGAGAGGAATCTTGCGGGCATATTTTGATCCTCTGCCTCCCC 2382	CAATATTGACACTGGTAAAGCAGAAATACTTGGATTCATTTACTCCATGCTGGTTAAATC 2322 	TTCAGAAACCATTATTGATTTGTTCAGTGATGAGGCACTGTAAATCCTCAATATAAAAAAG 2262 	ATGCACTACTGGAAATGTTTCCGGAAATCACTGTGGAAAATCTTCCCAGTTATTTCAGAC 2202 	AAATAGAGAGCATCCCACTAGCTAGCACACATGCACAAGACATAGTTCAAATAATAACAG 2142

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McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Plsani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Plsani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Taigilio, J., Tesfalye, S., Theodore, J., Tirell, A., Travers, M., Trigilio, J., Tesfalye, S., Theodore, J., Tirell, A., Travers, M., Trigilio, J., Travers, M., Trave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-MAR-2000) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2000 this sequence version replaced gi:7651991. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0, 960731
Consensus quality: 153679 bases at least Q40
Consensus quality: 157422 bases at least Q30
Consensus quality: 158798 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 153700; sum-of-contigs
Quality coverage: 5.1 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-contigs
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------ Project Information
Center project name: L7940
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Chemistry: Dye-terminator Big Dye:
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39181 4775
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3394 3493: gap of 100 bp
3494 8261: contig of 4768 bp in length
8262 8361: gap of 100 bp
8362 13937: contig of 576 bp in length
13938: 14037: gap of 100 bp
14038 23507: contig of 9470 bp in length
                                                                                                                                                                                                                                                                                    338 23507: contig of 9470 bp in len
308 23607: gap of 100 bp
308 30363: contig of 6756 bp in len
308 30463: gap of 100 bp
304 39480: contig of 8617 bp in len
308 30363: contig of 8617 bp in len
309 30980: contig of 8573 bp in len
309 30980: contig of 8573 bp in len
301 39180: gap of 100 bp
302 47853: gap of 100 bp
303 47853: gap of 100 bp
304 47853: gap of 100 bp
305 4771: gap of 11656 bp in len
307 71027: contig of 11656 bp in len
308 3080: gap of 100 bp
308 84959: contig of 11832 bp in len
308 3080: gap of 100 bp
308 3080: contig of 11832 bp in len
308 3080: gap of 100 bp
308 3080: contig of 11832 bp in len
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108075: contig of 12487 bp
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contig of 15085 bp in
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Best Local Similarity
Matches 1997; Conserv
                                        114776 TTGAAACTCTGAGAATAAAGCATTGGAATAGAAGTAATTGGTTTAAAGAAGCAGAAAAAT
                                                                                              114716
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140494. .161100
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108176. .123260
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85060. .95488
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/db_xref="taxon:9606"
/clone="RP11-263N17"
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71128. .84959
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99.88;
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Web site: http://www.genoscope. Contact: SeqRef@genoscope.cns.f

e.cns.fr/ .fr

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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 5 CNSO1RGG LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Qy 4435 P Db 113036 P Qy 4495 Q Db 112976	Qy 4315 1 Db 113156 3 Qy 4375 1 Db 113096 1	Qy 4195 c Db 113276 c Qy 4255 1 Db 113216 1	Qy 4075 7 Db 113396 7 Qy 4135 C Db 113336 C	Qy 4015 1 Db 113456 1
	CNSO1RGG 176368 bp DNA linear PRI 13-NOV-2001 Human chromosome 14 DNA sequence BAC R-933I1 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence. AL157971.4 GI:16944346 HTG. human Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 176368) Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,	ACCTTTGTCAGCAATTTTGACAGTCATTAATGTTTGTCATAATTTAAAAAAGTGTCTG 4494	TGGGAACAATGAGAGTGAACTCTAAATATAGGTTGTAGTAATAAAACATCATTAGCCTAA 4374	GTGCATMTATTTCCTTATAACATAGACCCGTTGCTACTCTCAGCACCCTCTCCTCAATTT 4254 :	TTTTCTTTTAATATCTACTTGATATCTTGTTGTTTAAATTTTCTTCACATATGGTTTG 4134	TTTGCTCTGTGCATTTTTTGAGACATTTGTTGAGAATATTCTATTTGGTGCTCTACTGTA 4074

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Best Local Similarity
Matches 1997; Conserva
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/db_xref="taxon:9606"
/chromosome="14"
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4074 155893	TTTGCTCTGTGCATTTTTTGAGACATTTGTTGAGAATATTCTATTTGGTGCTCTACTGTA	4015 155834	. Qy
4014 155833	TITCATTCCAAATCACTTAGCTGTTAGACTGATCTGTTTGTAGCAGTTGTTTGT	3955 155774	Qy Db
3954 155773	TCTCCCTGAGCCACACGGCCTCATTCTGTGAGGGAGAGAATAAGCCAAAGAGTTAAT	3895 155714	Qy Db
3894 155713	GCTCCCTCATCTGAAGCGTCTCTGAAATCTACCCTTGCAAGCTTCAGACAAATCAGTTGA 	3835 155654	Qy Db
3834 155653	TGGCTAAATTTCAGATTGAACAGGGATTCAGCATTCTGCCATCTCCTCATGGAAAGAGAG	3775 155594	Qy Db
377 4 155593	CAGAATGATATTTATATTTTAAGTGAGTCTTAAAACCTCCTCTTATTTTCTACAAGTTATA	3715 155534	Qy Db
3714 155533	ATACAACTTGATCTTTTCTAATATTTTCAGAAAGTGATGGGATAACCCTAGAAGAGGGACT	3655 155474	Qy db
3654 155473	TGAAAAAATTTTGGCTATTAAAGATATGTATTAGATGGTCTTATCCTGATTATTACCTGG 	3595 155414	Qy dd
3594 155413	AAAGTAACCTGTGGCAGACTAGGTTTCCAGAATTTCCTGGTTCTGCTCACGTATCATGTT	3535 155354	Qy Db
3534 155353	CAACAAAGAATTATCCTGCCCGAAATGGTAGTCGTGCCAAGGCTGAGTAACCTTGTGTTA 	3475 155294	Qy
3474 155293	GACATTTAGTGAGTAGAGGCCATGGATCCTGCTAAATAACCTGCATTGGACAGCGCCCCA 	3415 155234	Qy Db
3414 155233	TCAGGGGATATTTAGCAATTGTCGGGAGACATTTTTGATGTCATGACTAGGGCAGTTATT	3355 155174	Qy Db
3354 155173	CAGCTGACAGTTATATTTGTTTTATTGGAGTCATGATATTAAAATCAGCGTTTGTCAACC	3295 155114	Qy Db
3294 155113	TGATTTCTATTTGGATTAAAATTAAACTCTAATCACAGTTAACTCCACAGTGCATTCATG	3235 155054	Qy Db
3234 155053	TACTGTATTGGACAGTTCAGTACTAGACAAAAACTAGCATAATTAACTTAGTTCTAGCCA 	3175 154994	Qy Db
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                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIML at; http://image.llnl.gov Series: IRAK Plate: 54 Row: d Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                               Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                       analysis
                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: BCM-HGSC
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
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                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                Location/Qualifiers
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Martin, R.G.,
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                                      GACGTGATAAAGAGTTAGGATGCTCAAAAGTGAACTAATTTTATAGGGCTGTGGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTCTGCCCAGGAATGGAAACCTCCTCTTCCTGCTTTGATTTCTGAATATGATGGACG
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                                                                                        CTCTCTGTGGCACAGGAAACCCGAGATCAAATCTGTAAAGGAACAGGACTAAATTATGCC
                                                                                                                          AAATTTTTTTGGCATGATAGACTTAATTTATTTCCTTAAAGAATAATATTAAATCATTTC
                                                                                                                                                                ACCACGACAAGGAGTTATGAGCGG-----
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HSGGQYYAFPSSQSYTEQSLVLWLKHLQAGLENPITVLSAQEWKPPLPAFDFLNMMDA
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FHHDKEL"
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                                                                               Score 426.4; DB 10;
Pred. No. 1.2e-75;
0; Mismatches 326;
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                                                                                         Sequencing vector: M13: 100%
Sequencing vector: M13: 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 19295 bases at least Q40
Consensus quality: 195796 bases at least Q30
Consensus quality: 195746 bases at least Q20
Insert size: 209000; agarose-fp
Quality coverage: 4.50 in Q20 bases; agarose-fp
Quality coverage: 4.58 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTACTTCCGAGTAGCCATATTTCAAGTGTTCATTGCCACATGTGGCCTGTGACTACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204606 bp DNA linear HTG HOMO sapiens chromosome 14 clone RP11-382I20, WORKING DR SEQUENCE, 27 unordered pieces.
AC02I131 SGI:8569986 HTG; HTGS_PHASEA ...
                                                                                                                                                                                                                                                                                                                                           Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center code: WUGSC
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Direct Submission
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The sequence of Homo sapiens
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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 204606)
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                                                        /note="assembly_name:Contig15"
4334. .6059
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2627. .4233
 /note="assembly_name:Contig17"
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                                                                                                                                                                                           /clone="RP11-382I20"
                                                                                                                                                                                                                /chromosome="14"
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/db_xref="taxon:9606"
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TCTCAGCACCCTCTCCTCAATTTTTTTTCCTGTAGCATGTGATGCCTGATTAAACTCATT
                                                        AAATTTTCTTCACATATGGTTTGCCTGATACAACTGATTTTTATAACTGAAATTTAAGGA 4171
                                                                                      ATCTAACAGCTAAAACTCAGTAAGTGCATMTATTTCCTTATAACATAGACCCGTTGCTAC 4231
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164004. . 204606
/notce="assembly_name:Contig39"
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42826. 48145
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37324. .42725
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33717. .37223
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29918. 33616
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136451. .163903
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77844. .88107
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11733. .14000
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26003. .29817
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            CCTCAGAAATATTTTAGTACATTGCAACCAGG 502
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                                                                                                                                                                                                                                                                                                                                 348;
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Sequence 34(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptides and methods for the Patent: WO 0107611-A 340 01-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc. (US)
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               204606 bp DNA linear HTG 07-HOMO sapiens chromosome 14 clone RP11-382I20, WORKING DRAFT SEQUENCE, 27 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 4.50 in Q20 bases; agarose-fp Quality coverage: 4.58 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.H.
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, 27 unordered AC021131
AC021131.5 GI:8569986
HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jun 16, 2000 this sequence version replaced gi:7534281.
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                                                                                                                                   /note="assembly_name:Contig24"
33717, .37223
                                                                                                      /note="assembly_name:Contig27"
48246. .52585
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29918. .33616
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26003. .29817
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                                                                                                                                                                                                                                                       /note="assembly_name:Contig20" 17073. .21089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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48145: contig of 5320 bp in ler
48245: gap of unknown length
52585: contig of 4340 bp in ler
52685: gap of unknown length
52585: contig of 5711 bp in ler
58496: gap of unknown length
64865: contig of 6369 bp in ler
64965: gap of unknown length
64965: gap of unknown length
70722: contig of 6921 bp in ler
70822: gap of unknown length
77743: contig of 6921 bp in ler
77843: gap of unknown length
88107: contig of 10264 bp in ler
77843: gap of unknown length
88107: contig of 11366 bp in ler
99443: gap of unknown length
112627: contig of 11384 bp in ler
112727: gap of unknown length
112627: contig of 1279 bp in ler
1125106: gap of unknown length
1136350: contig of 11244 bp in ler
1136450: gap of unknown length
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1164003: gap of unknown length
164003: contig of 127453 bp in ler
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 AGAAACCAT-TATTGATTTTGTTCAGTGATGGCACTGTAAATCCTCAATATAAAAAAG--
                            NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTCGTAGACTTCTTGGTTT
                                                         CACTACTGGAAATGTTTCCGGAAATCACTGTGGAAAATCTTCCCAGTTATTTCAGACTTC 2205
                                                                                                                 TAGAGAGCATCCCACTAGCTAGCACACATGCACAAGACATAGTTCAAATAATAACAGATG
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38935 c 39288 g 59611 t
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125107_ .136350
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88208. .99343
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77844. .88107
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164004. .204606
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136451. .163903
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99444. .112627
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Pred. No. 1e-36;
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AUTHORS
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1 (bases 1 to 212103)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottler,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J. Sequencing of the human chromosome 14

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS01DV4 212103 bp DNA linear PRI 01-JUN-21
Human chromosome 14 DNA sequence BAC R-841020 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.

    Web: www.genoscope.cns.fr)
    On Jan 12, 2001 this sequence version replaced gi:7009594
    ----- Genome Center

                                                                                                                                                                Overall
                                                                                                                                                                                                               Quality
                                                                                                                                                                                                                                              The following BAC sequence is oriented ..... Summary Statistics
                                                                                                                                                                                                                                                                                                                             Center: Genoscope / Centre National de Center code: GS
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.
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AL133453.3 GI:12140277
                                                                                                                                                                                                            Assembly program: Phrap; version Quality coverage: 8.52x in Q20 ba
                                                                                                                                                                                                                                                                                             Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Best Local Similarity 99.5%;
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                                                                                                                                                                                      TATTTTAGTACATTGCAACCAGG 502
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                                                                                                                                                                    TATTTTAGTACATTGCAACCAGG 6582
                                                                                                                                                                                                                                                                 ATAATGTGCATTTTTACATGCCAACAGTAAACTCTTTACCAGAACTGAGTCCTCAGAAA 479
                                                               AC102579 203610 bp DNA Mus musculus clone RP23-248E1, WORKING
   AC102579.2
HTG; HTGS_P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identified using the e-PCR software (G. Schuler) ^{\rm m} 65366 a 40917 c 40188 g 65632 t
2579.2 GI:22381563
HTGS_PHASE1; HTGS_I
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RHdb:RH80771
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RHdb:RH100282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="matching EMBL:G37390
RHdb:RH101245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                  DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1
                                                                                                                                                                    Center code: WIBR
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Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McDrbu, C., Mandonald, P., Major, J., Marquis, N., Maylor, J., Nguyen, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McDrbu, C., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Enbritted, J., 21 Mmer, A. and Zody, M.
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2 (bases 1 to 203610)

2 (bases 1 to 203610, Nusbaum, C., Lander, E., Ali, A., Allen Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhga Anderson, S., Barna, J., Campopiano, A., Chang, J., Chazaro, B., Company, A., Coalins, S., Collymore, A., Cook, P., Cock, P
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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Birren,B., Nusbaum,C. and Lander,E.
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarrata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., 1liev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Neneus, L., Mihova, T., Minga, V., Murphy, T., Naylor, J., Neell, D., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Viel, R., Voa, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Shahert, S., Chupback, L., Zimmer, A. and Zody, M. to 203610)

Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061665. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html

------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Contact: sequence_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu

Center project name: 248_E_1
Center clone name: 248_E_1
Center clone name: 248_E_1
Center clone name: 248_E_1
Center clone name: 248_E_1
Center clone: Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Hig Dy: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 194595 bases at least Q40

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13001 13100: gap of 1918 bp in length
13001 13100: gap of 1918 bp in length
15019 15118: gap of 1918 bp in length
1774 17373: gap of 100 bp
1774 17373: gap of 100 bp
1774 17373: gap of 100 bp
1774 21030: contig of 3657 bp in length
17374 21030: contig of 3657 bp in length
17374 21030: gap of 100 bp
17374 2493: gap of 100 bp
17385 27384: gap of 100 bp
17385 53071: contig of 2791 bp in length
153072 53171: gap of 100 bp
153172 55684: gap of 100 bp
153172 55684: gap of 100 bp
16385 6684: gap of 100 bp
17385 6684: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 198128 bases at least Q30 Consensus quality: 199686 bases at least Q20 Insert size: 204000; sum-of-contigs quality coverage: 6.3 in Q20 bases; agarose-fp Quality coverage: 6.4 in Q20 bases; sum-of-contigs
178519 178618: gap of 100 bp
178619 201081: contig of 22463 bp in length
201082 201181: gap of 100 bp
201182 203610: contig of 2429 bp in length.
                                                                                                                                                                                                                                                        151351 151450: gap of
151451 163581: conti
163582 163681: gap of
163682 178518: conti
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129793 141332: contig of 11540 bp in length
141333 141432: gap of 100 bp
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97780 97879:
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3945 4044: gap of 100 bp
4045 5485: contig of 1441 b-
5486 5585: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71336 71435:
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1367 1466: gap of 100 bp
1467 2392: contig of 926 bp in length
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2392: gap of 100 bp
493 3944: contir - 945 4044
                                                                                                                                                                                                                                     1450: gap of 100 bp
163581: contig of 12131 bp in length
33681: gap of 100 bp
178518: contig of 14837 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6141: gap of 100 bp 10 length 1879: gap of 100 bp 106798: contig of 8919 bp in length 16898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129692:
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71335: contig of 7287 bp in length
435: gap of 0bp
78031: contig of 6596 bp in length
131: gap of 100 bp
86041: contig of 7910 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp 103948: contig of 7264 bp in length 8: gap of 100 bp 1335: contin of 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of 100 bp
0: contig of 9918 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of 100 bp
2: contig of 8623 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 14071 bp in length
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FEATURES

Location/Qualifiers

RESULT 12 AC102579/c LOCUS AC102579 DEFINITION Mus muscul pieces. ACCESSION AC102579 VERSION AC102579.2	1751	Qy 1691 TAAGCAAAATG Db 135407 GAACCAAAATG	QY 1631 AGGCACATCTA	Query Match Best Local Similarity Matches 145; Conser	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	c_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature		source
203610 bp DNA linear HTG 21-AUG-2002 Llus clone RP23-248E1, WORKING DRAFT SEQUENCE, 29 unordered 2 GI:22381563	+ (TAAGCAAAATGTTACTGAATTTCCTATCATAAAGATGTACAAGAAAGGCGAGAACCCAGT 1750 	AGGCACATCTACTATGCTTCTTACTAGAATAAACTGTGCAGATTGGTCTGATGTATGT	2.9%; Score 129.4; DB 2; Length 203610; larity 84.8%; Pred. No. 1.1e-15; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	710ce="assemory_fragment" 97880106798	ssembly_fragment	_tragment	assembly_fragment.78031	/note="assembly_tragment" 6404971335	assembly_ .63948	.56584	assembly_t .53071	, Ita	, ;	L III	,	, [1	-"assembly_f .10621	<pre>/note="assembly_fragment" 69168703</pre>		,	LITE	side:left .2392	<pre>/clone_lib="RPCI-23 Female Mouse BAC" 11366</pre>	/db_xref="taxon:10090" /clone="RP23-248E1"	1203610 /organism="Mus musculus"

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS Birren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barran, B., Nusbaum, C., Lander, B., Choepel, Y., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zembek,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Nusbaum, C
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                                                 Center clone name: 248_E_1
Center clone name: 248_E_1
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector Plasmid; n/a; 100% of reads
                                                                                                                                                                                                  Center project name: 24
                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                          http://www-seq.wi.mit.edu
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rminator Big Dye; 100% o Phrap; version 0.960731
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runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 6.3 in Q20 bases; Quality coverage: 6.4 in Q20 bases;
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64048: gap of 100 bp
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13000: contig of 279 bp
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                   HS503N11 94749 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from clone 503N11 on chromosome 6p24.1-24.3. Contains an STS, GSSs, genomic amrker D6S470 and a ca repeat
    polymorphism, complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 126.6; DB 2; Pred. No. 4.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was generated from part of bacterial clone contigs human chromosome 6, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 503N11 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone 503N11. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
On May 13, 1999 this sequence version replaced gi:4581366.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-MAY-1999) Sanger Centre, Hinxton, Cambri
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 94749)
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AL031122.3 GI:4826502
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    complement(12911. .1333)
/note="match: GSS B40033"
/note="match: GSS B40033"
/note="match: GSS B40033"
                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS AQ150392"
5820. .6049
/note="MIR repeat: matches 35. .262 of consensus"
6184. .8869
/note="LIMB5 repeat: matches 2923. .5873 of consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 15. .259 of consensus" 3192. .3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER5A repeat: matches 100. .188 of consensus" 2774. .2997
                                                                                                                                               11832. .11914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="p24.1-24.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                      /note="L1MA5A repeat: matches 6152. .6292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP3-503N11"
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                                                                                                                         note="MER91B repeat: matches
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copies 2 mer gt 92% conserved
                                                                                                                                                                repeat: matches
                                                                                                                                                                  674.
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/note="23 cop:
15594. .15633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 59.
complement(31515. .31877)
/note="match: GSS AQ100296"
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/note="match: GSS B33497"
20807..20985
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complement(17752. .18167)
/note="match: GSS' AQ065232"
                                                    /note="MER63B repeat: matches 8.
38376. .38542
                                                                                                      'note≖"L2 repeat: matches 2089.
                                                                                                                                                                      'note="Charlie5 repeat: matches 2289. .2574
                                                                                                                                                                                                                         'note="16 copies of ca 100% conserved; differs
                                                                                                                                                                                                                                          /note="match:STS Z24589; genomic marker D6S470"
35348. .35379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="LTR12 repeat: matches 14. .1440 of
                                                                                                                                                                                                                                                                                                                                                                                         'note="Charlie5 repeat: matches 7. .291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                          te="L2 repeat: matches 1729.
                                                                                                                                                                                                                                                                                       e="L1MA10 repeat: matches 5994. .6316 of consensus"
                                                                                                                                                                                                                                                                                                                        e="Charlie5 repeat: matches 901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="L2 repeat: matches 2675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="12 copies 2 mer tt 96% conserved"
1. 21393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="LTR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        j="MLTIA1 repeat: matches 1. .337 of consensus"
). .20418
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1. .24675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e="match: GSS AQ348225"
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20512
 repeat: matches 2310.
                                                                                                                                     copies 2 mer aa 96% conserved"
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                                  repeat: matches 133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 5851. .6181 of
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2.7%;
Best Local Similarity 55.9%;
Matches 378; Conservative
                                                        65454 TCTTTTACTTTTTAAAATACAAAGTCCTTGAAATTGGTGTTTTATACTCCCAACA 65513
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                                                                                                                                                                                                                                                                                                       65275 GAACAGAACCATCCAATACAAGTATAATGCAAATCACTTATGTAATTTCAAAATTCTCCAG
                                                                                                                                                                                                                                                 2950 TAACTACATTAAACAAAGTAAAAGTGAGGCAGGGCAAAATAATTTTGATATTTACTTTTCAC
                                                                                                                                                                                                                                                                                                                        2890 GACTAGTGCCATCCAATAGAATTATAATATAATATATATTTTATTTTAAAATTTTTCTAG
                    3118 TTTCTTACTTCCGAGTAGCCATATTTCAAGTGTTC-ATTGCCACATGTGGCCTGTGACTA 3176
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                                                                                                 CCA--GTAGTATACCCAAAATAGCGAAAT-----ATAGAAATTATTAATGAGATA 3057
49830...50123
/note="Alusc repeat: matches 16...309 of consensus"
50124...52184
/note="TIGGER1 repeat: matches 273...2417 of consen
52185...52247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complement(52938. .53361)
/note="match: GSS AQ185926"
54150. .54465
/note="LIMA7 repeat: matches 5963. .6288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /uute="MER2 repeat: matches 15. .342 of consensus" complement(52938. .53361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat:
49549. .49829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39184. .39447
/note="AluSx repeat: matches 38.
39451. .39832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 198. .259
52873. .53187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS AQ167854"
46563. .46893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="26 copies 2 mer aa 71%
46301. .46562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluY repeat: matches 1. .305 of consensus"
43559. 43959
/note="AluSg repeat: matches 1. .305 of consensus
44272. .44367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 55.
41558. .41862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="TIGGER1 repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1PA7 repeat: matches 5706. .6143 of consensus"
15926. .45977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1P repeat: matches 558. .961 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="L2 repeat: matches 1901. .2131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER2 repeat: matches 1. .345 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MIR repeat: matches 1. .258 of consensus"
|5488. .45925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="L2 repeat: matches 2598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="L2 repeat: matches 1555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MLT11 repeat: matches 245. .410 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 47.
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Pred. No. 1.4e-14;
0; Mismatches 260
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Consensus quality: 6526 bases at least Q40 Consensus quality: 11341 bases at least Q20 Consensus quality: 11249 bases at least Q20 Consensus quality: 12249 bases at least Q20 Estimated insert size: 124000; pulse field gel estimation Estimated insert size: 13599; sum-of-contigs estimation Quality coverage: 0.14 in Q20 bases; pulse field gel esti Quality coverage: 1.28 in Q20 bases; sum-of-contigs estin * NOTE: This record contains 10 individual * sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Joint Genome Institute Center Code: JGI
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Sequencing of Human Chromosome
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Homo sapiens chromosome 5 clone
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ive, Walnut Creek, CA
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/db_xref="taxon:9606"
/chromosome="5"
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Submitted (31-0CT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 89196)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Homo sapiens chromosome 5 clone CTD-2022K1, complete sequence.
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Matches 208; Conserv
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                                 CTGGACAGCACAGTTCTAG
                                                                                    TTGGACAGTTCAGTACTAG 3200
                                                                                                                                                                            TACTTCCGAGTAGCCATATTTCAAGTGTTCA-TTGCCACATGTGGCCTGTGACTACTGTA
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Conservative

2.2%;

Score 97.8; DB 4; Pred. No. 7.5e-15; 0; Mismatches 102;

Length 6792;

9 Gaps

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RESULT 1 US-09-374-45 Sequence 2 Patent No. GENERAL IN APPLICANT APPLICANT TITLE OF FILE REFE CURRENT F CURRENT F EARLIER A CURRENT F EARLIER F NUMBER OF SOFTWARE SOFTWARE SOFTWARE US-09-374-45		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
54 - 254 - 254 - 254 - 254 - 254 - 255 - 2		533 533 533 533 533 533 533 533 533 533
54-20 20, Application 20, Application 6395548 NFORMATION: T: Lee, Mu-En T: Hsieh, Chung TI: Hsieh, Chung TI: Hsien Chung TENCE: 05433/ APPLICATION NUP FILING DATE: 19 APPLICATION NUP FILING		11.000
4-20 0, Application US/0937 6395548 FORMATION: 1 Lee, Mu En 1 Hsieh, Chung Ming INVENTION: METHODS OF PPLICATION NUMBER: US/ ILING DATE: 1999-08-13 PPLICATION NUMBER: US SEQ ID NOS: 22 PastSEQ for Windows V 20 6792 6792 HOMO Sapiens		176373 50000 1750 13865 13865 13865 138247 19124
/09 /09 /01 /08 /08 /08		344334224142215134
Application US/09374454 pg5548 MATION: MATION: MATION: Mee, Mu-En Idemura, Koji Idemura, Ming Idemur	ALIGNMENTS	US-09-128-155-17 US-09-146-053-3 US-09-276-531-34 US-09-009-217-11 US-09-009-217-11 US-09-345-882-1 US-09-014-969-14 US-09-659-791A-10 US-08-813-795A-36 US-08-883-795A-36 US-08-628-417-6 PCT-US-3-07261-10 US-08-319-704-5 US-08-319-704-5 US-08-319-704-5 US-08-319-704-5 US-08-319-704-5 US-09-209-668-8 US-08-482-073-7
ES1S		Sequence 17, Appli Sequence 34, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 14, Appli Sequence 10, Appli Sequence 10, Appli Sequence 36, Appli Sequence 36, Appli Sequence 13, Appli Sequence 10, Appli Sequence 10, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli

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RESULT 2
US-07-906-871-15/c
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US-07-906-871-15
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Best Local Similarity
               Query Match
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APPLICANT: Stevens,
APPLICANT: Avraham,
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
                                                                                        FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE: 13-JUL-
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                   LENGTH: 17327 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
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                                                                            NAME/KEY:
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Shalom
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Score
Pred.
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91.4; DB 1;
No. 5.3e-13;
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              Length 17327;
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US-09-784-316-3
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Best Local
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SOFTWARE: FastSEQ for
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                              Matches 188;
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TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL001139
CURRENT APPLICATION NUMBER: US/09/784,316
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                   22230 TCCAATAGAAATATAATGTCAGTCATACACATAATTTAAAAATTTCTACTAGCCACATTA 22289
                                                                                                                                   22348
                     3134
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AGCCATATTTCAAGTGTT-CATTGCCACATGTGGCCTGTGACTGTATTGGACAGTTC
                                                       GTTCTGCATCCTCAAAATGCCAAATGCATTCTATACTTACATCACATCTCGATCCAAACT
                                                                           CCCAAAATAGCGAAATATAGAAATTATTAATGAGATATT-----TTACATCCTTTTTT 3073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCTGTCCCAATTTGCCTTGGCCACATTTCAAGTGTTCAGTAGCCACAAGTGACTTGTG
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Pred. No. 1.9e-08;
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                                                                                                                                                                                          Sequence 79, Patent No. 6
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Best Local Similarity
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                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                      APPLICANT:
                  CORRESPONDENCE ADDRESS
                                                                                                                        APPLICANT:
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ADDRESSEE:
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64102
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                                                                                                                                                                                                                                                                                                                                                                                                           AATGCAGTACATATTTTATACTTACTGCATTTCTTACTTCCGAGTAGCCATATTTCAAGT 3148
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAATTATAACCAAATTAAAATTAAGGAGATATTTTACAATTTTCATATTAACGTTTCCA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGTTGAAATAAATTTTAATATCTTTCATTGAACCCAATATATGCAAAATACTATCATT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGGGCAAAATAATTTTGATATTACTTTTCACCCA-----GTAGTATACCCAAAAT 3028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACAAGCTGCATATGTAATTTAAAATTTTCTAATAACCACATTTAAAAAAGGTAAAAAGAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTGTAGAATGTGACTTGC 22547
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                                                                                                                                                                                                                                                                                                    GCTCAACAGCTACGTGAGGATAGTGGCTATTATGTCACAAAATGCAGCTCTA 327
                                                                                                                                                                                                                                                                                                                                                                          ATTCTGGTGTGAATTTTACACTCACCGAACATCTCAATTCTGACAAGTCATATTTTAAGT
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                                                                                                                                                                                                             Application US/08781891
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                                                             Mulligan, John T.
Schellenberg, Gerald D.
SCHELLENBERG, GENE PRODUCTS RELATED TO
                                                                                                                      Oshima, Junko
                                                                                                                                        Yu, Chang-En
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SEED and BERRY LLP
                                                                                                                                                           Ying-Hui
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                                 WERNER'S SYNDROME
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Pred. No. 9.6e-09;
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RESULT 6
US-09-791-211-3
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                                                                                            SEQ ID NO 3
                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                    APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0205
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 79: SEQUENCE CHARACTERISTICS:
                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45829 CAGTAGAAATACAATGTGAGCTACATATGCAATTTTAAATTTTCTAGTAGCCACATTTTA 45888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45889 AAAAGTAAATGGATGCAATTTATTTTGATAATATAATTTAATTTAGTCTACTATATTTTAAA 45948
FEATURE:
NAME/KEY: unsure
                                                             LENGTH: 87543
TYPE: DNA
                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   3010 CCAGTAGTATACCCAAAATAGCGAAATATAGAAATTATTAATGAGATATTTTACATCCTT 3069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2963 CAAAGTAAAAGTGAGCAGGGC------AAAATAATTTTGATATTACTTTTCAC 3009
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 1.5%;
Local Similarity 62.7%;
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CITY: S
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39,317
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Gaps

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OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 7427 LOCATION: 7421

unknown

NAME/KEY: unsure LOCATION: 12605 OTHER INFORMATION:

unknown

NAME/KEY: unsure LOCATION: 12742 OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 29370 OTHER INFORMATION:

unknown

NAME/KEY: unsure LOCATION: 11609 OTHER INFORMATION: unknown

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US-09-791-211-3
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Best Local S
Matches 148
                                                                                                               46022
                                                 46082 AAAAGTAAATGGATGCAATTTATTTTGATAATATAATTTAATTTAGTCTACTATATTTTAAA 46141
                                                                                                                                                                                                                                                                                      NAME/KEY: unsure LOCATION: 86336
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: unknown NAME/KEY: unsure LOCATION: 79198
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LOCATION: 68739
OTHER INFORMATION:
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LOCATION: 68660
OTHER INFORMATION:
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LOCATION: 66614
OTHER INFORMATION: unknown
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LOCATION: 59242
OTHER INFORMATION: unknown
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LOCATION: 52787
OTHER INFORMATION: unknown
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LOCATION: 52786
OTHER INFORMATION:
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OTHER INFORMATION: unknown
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3010 CCAGTAGTATACCCCAAAATAGCGAAATATAGAAATTATTAATGAGATATTTTACATCCTT
                                                                                                             7 Match 1.5%;
Local Similarity 62.7%;
nes 148; Conservative
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Pred. No. 5.8e-07;
0; Mismatches 73;
                                                                          -AAAATAATTTTGATATTACTTTTCAC
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NAME/KEY: unsure LOCATION: 30140 OTHER INFORMATION: unknown

OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 30136

OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 29981

OTHER INFORMATION: unknown NAME/KEY: unsure LOCATION: 29980

OTHER INFORMATION: unknown

OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 29422

NAME/KEY: unsure LOCATION: 29979

NAME/KEY: unsure LOCATION: 31205 OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 39020 OTHER INFORMATION: unknown NAME/KEY: unsure LOCATION: 42164

OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 42459

NAME/KEY: unsure LOCATION: 36816 OTHER INFORMATION:

unknown

OTHER INFORMATION: unknown NAME/KEY: unsure LOCATION: 34072 OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 34066

OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 33160

NAME/KEY: unsure LOCATION: 33095

OTHER INFORMATION: NAME/KEY: unsure LOCATION: 31592

unknown

OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 31206 OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 46808 OTHER INFORMATION: unknown

OTHER INFORMATION: unknown

Gaps

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3069

OTHER INFORMATION: NAME/KEY: unsure

unknown

unknown

NAME/KEY: unsure LOCATION: 46826 OTHER INFORMATION: NAME/KEY: unsure LOCATION: 46823

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; OTHER INFORMATION:
US-08-724-394A-20
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Best Local Similarity
Matches 157; Conserv
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154849 ATTAAAATATTGAGTTTTTACTTTGTTATTTTACTAGTTCTTTGAAATCTGGTGTGTATT 154790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                      2984
                                                                                                                                                       2924 CACATATTTTATATAAATTTTCTAGTAACTACATTAAACAAAGTAAAAGTGAGGGC 2983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
                              3044 TTATTAATGAGATATTTTACATCCTTTTTTGTACCAAGTCTTCTAAATGCAGTACATATT 3103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1..246240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08
FILING DATE: 01-OCT-1996
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                                                                                                   AAAATAATTTTGATATTACTTTTCACCCAGTAGTATACCCCAAAATAGCGAAATATAGAAA 3043
                                                                  AATCTATTTTAATGATTTGAATCCAGTGTAACCAAAAATTGTTTCAACAAGGTATCTAAT 154850
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Wolff, Roger K.
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                      Score 65.2; DB 2;
Pred. No. 1.1e-05;
0; Mismatches 108
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                                                                                                                                 Query Match
Best Local Similarity
Matches 157; Conserv
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                                                                    154963 CACATATGTAATTTTAAATTTTTAATAGGCACATTTTA-
154909 AATCTATTTTAATGATTTGAATCCAGTGTAACCAAAAATTGTTTCAACAAGGTATCTAAT 154850
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 415-576-0200
                                 2984 AAAATAATTTTGATATTACTTTTCACCCAGTAGTATACCCCAAAATAGCGAAATATAGAAA 3043
                                                                                                       2924 CACATATTTTAATTTAAAAATTTTCTAGTAACTACATTAAACAAAGTAAAAGTGAGCAGGGC 2983
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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Pred. No. 1.1e-05;
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                                                                                                     Query Match
Best Local Similarity
Matches 157; Conserv
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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                                                    2924 CACATATTTTATTTAAAATTTTCTAGTAACTACATTAAACAAAGTAAAAGTGAGCAGGGC 2983
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: Two Embarcadero Center, 8th Floor
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REFERENCE/COCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /no
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Lauer, Peter M.
                                                                                                         Conservative
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Tsuchihashi, Zenta
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                                                                                                                     1.48;
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                                                                                                     Score 65.2; DB 2;
Pred. No. 1.1e-05;
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; OTHER INFORMATION: Incyte ID No. 6426186 331395.1CB1
US-09-484-970B-44
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SOFTWARE: PERL PROGRAM
SEQ ID NO 44
LENGTH: 2821
TYPE: DNA
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Best Local Similarity
Matches 207; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMC
FILE REFERENCE: PB-0014 US
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CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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                                                                                                                                                                                                                                                                                                                                                                           CATATTTCAAGTGTTCATTGCCACATGTGGCCTGTGACTGTATTGGACAGTTCAGTA 3196
                                                                                                                                                                                                                                              TATACCCAAAATAGCGAAATATAGAAATTATTAATGAGATATTTTACATCCTTTTTTGTA 3076
CTATACTCATTCCTTCAAA 1424
                                   CTAGACAAAAACTAGCATA 3215
                                                                                                                                                  TTAGGCCTTTGAAATTCAGTGTGTATTAAACA-----CATCTCAATTCAAACCATCAC
                                                                                                                                                                                   CCAAGTCTTCTAAATGCAGTACATATTTTATACTTACTGCATTTCTTACTTCCGAGTAGC 3136
                                                                                                                                                                                                                            CATTTCAACATAGGATCAATATAAAAATTATTAATGAGTTATTTTACTT--TTTTTCATA
                                                                                                                                                                                                                                                                                                    AAAGAACCCAGGTATTGATTTAAATATTTATTTTAACCCCAATAGGCTCAAAAACACTAT 1234
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                                                                        CATATTTCAAGTCTTTGTAGCCAAATGTGACTAGTGGCTACCATATTAGACAGTGCAGAT 1405
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Pred. No. 2.2e-06;
0; Mismatches 147;
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RESULT 12
US-09-641-638-24/c
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PRIOR APPLICATION NUMBER: US 09,
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 09,
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
                                         GENERAL INFORMATION:
                                                                Sequence 24, Application US/09641638 Patent No. 6432648
                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.4%;
Best Local Similarity 64.9%;
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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
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                     APPLICANT:
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  APPLICANT:
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LOCATION: 266..286
OTHER INFORMATION: downstream
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OTHER INFORMATION: 12-628-306 : polymorphic base
NAME/KEY: misc_binding
LOCATION: 479..497
OTHER INFORMATION: 12-628-306.misl, complement
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ORGANISM: Homo Sapiens
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LOCATION: 458..477
OTHER INFORMATION: 12-628-306.mis2, potential
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NAME/KEY: allele
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LOCATION: 764,..782
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                                                                                                                                                                                                             ACATGTGGCCTGTGACTACTGTATTGGACAGTTCAGTACTAGACAAAAACT 3209
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                                                                                                                                                                                                                                                                                                                                                                                                                                         111; Conservative
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o. 6432648
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Cohen, Annick
Bougueleret,
                 Blumenfeld, Marta
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Pred. No. 1.5e-06;
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Sequence 3, Application US/09813133A

Patent No. 6455294

GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTITILE OF INVENTION: NUCLEIC ACID MOLECULES ENC.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001173

CURRENT APPLICATION NUMBER: US/09/813,133A

CURRENT TILING DATE: 2001-06-06
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Best Local
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PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
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CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
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LOCATION: 271..291
OTHER INFORMATION: downstream
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LOCATION: 769..787
COTHER INFORMATION: upstream amplification primer,
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LOCATION: 479..498
OTHER INFORMATION: 12-628-311.mis2, potential complement
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NAME/KEY: allele
LOCATION: 478
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Pred. No. 1.5e-06;
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                                                                                                    HUMAN PROTEASE PROTEINS,
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NUMBER OF SEQ ID NOS:

US-08-370-319C-12

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Patent No. 555000.
Patent No. 555000.
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Best Local Similarity 70.0
Matches 112; Conservative
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                                                                                                                                      TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/272,351
FILING DATE: 8-ULY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TUMOR TUTLE OF INVENTION: REJECTION
TITLE OF INVENTION: REJECTION
TO SECULE SECTION 12
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hanson. No 595500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                    LENGTH: 4129 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/370,319C
FILING DATE: 10-JANUARY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM:
                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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805 Third Avenue
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Traversari, Catia; W 1fel, Thomas; Coulie, Pierre;
Boon-Falleur, Thierry; De Plaen, Etienne
VENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
                                                                    linear
                                                                                                                                                                                               (212) 688-9200
                                                                                                                                                                                                                                                                                                      18-MAR-1993
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The sequence is preceded by unsequenced portion of from kilobases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOON-Falleur, Thierry; De Plaen, Etlenne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PRO
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
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                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                 COMPUTER: IBM PS, OPERATING SYSTEM: SOFTWARE: Wordpe:
REFERENCE/DOCKET
                 NAME: Hanson, No. 6201111man D. REGISTRATION NUMBER: 30,946
                                                                         APPLICATION NUMBER: FILING DATE: 18-MA
                                                                                                                                FILING DATE:
                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                        CLASSIFICATION:
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805 Third Avenue
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Traversari, Catia; W Ifel, Thomas; Coulie, Pierre;
Boon-Falleur, Thierry; De Plaen, Etienne
VENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
VENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED
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Pred. No. 8.7e-06;
D; Mismatches 157;
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; OTHER INFORMATION: The sequence is preceded by an ; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3 ; OTHER INFORMATION: kilobases
US-09-224-834-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3824
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 53.9
Matches 200; Conservative
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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compugen Ltd
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10 US-09-742-312-3
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10 US-09-746-877-3446
9 US-10-229-124-3
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10 US-09-35-464-1
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1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3		1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.5	1.5	1.5
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Sequence 862, App	Sequence 18, Appl	Sequence 5, Appli	Sequence 1429, Ap	Sequence 10, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2422, Ap	Sequence 7988, Ap	Sequence 1462, Ap	Sequence 1462, Ap	Sequence 1462, Ap	Sequence 1415, Ap	Sequence 2355, Ap	Sequence 232, App	Sequence 314, App	Sequence 313, App	Sequence 315, App	Sequence 10, Appl	Sequence 2380, Ap	Sequence 164, App	Sequence 241, App	Sequence 1768, Ap	Sequence 243, App	Sequence 3, Appli

RESULT 1

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Sequence 1, Application US/09847046

Patent No. US20020068036A1

PATENT NEVERTION:
APPLICANT: Hevezi, Peter
APPLICANT: Mack, David
APPLICANT: Mack, David
APPLICANT: Milson, Keith E.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF PROSTATE AND/OR BREAST CANCER.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF PROSTATE CANCER.
TITLE OF INVENTION: MODULATORS
FILE REFERENCE: A-69199-1/DJB/JJD/AMS
CURRENT APPLICATION NUMBER: US/09/847,046

CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US/09/733,288
PRIOR FILING DATE: 2000-12-08

PRIOR APPLICATION NUMBER: US/09/687,576

AN

ALIGNMENTS

; LENGTH: 4526 ; TYPE: DNA ; ORGANISM: HOMO s US-09-847-046-1

sapiens

SEQ ID NO 1

PRIOR FILING DATE: 2000-10-13 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PatentIn version 3.1

Query Match 100.0%; Score 4525.6; Best Local Similarity 100.0%; Pred. No. 0; Matches 4526; Conservative 0; Mismatches

DB 10; Length 4526;

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1260 1260	CTTGGCGTCTTCTGGGAAAAGCAGGAGTTCTACTCTTGTTAAGGGACTCTTTGGAAGTGA	y 1201 b 1201	문항
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4500	TCAGCAATTTTGACAGTCATTAATGTTTGTCATAATTTTAAATAAA		Db
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4260	ATTTCCTTATAACATAGACCCGTTGCTACTCTCAGCACCCTCTCCTCAATTTTTTTT	4201	Qy
4200	ACAACTGATTTTATAACTGAAATTTAAGGAATCTAACGGCTAAAACTCAGTAAGTGCAT	4141	Db Db
4	tttaatatetaettgatatettgttetttaaatttteeteaeatatggtttgeetgat	80	Дb
4140	TTTTAATATCTACTTGATATCTTGTTCTTTAAATTTTCTTCACATATGGTTTGCCTGAT	4081	Qy
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4080	TGTGCATTTTTGAGACATTTGTTGAGAATATTCTATTTGGTGCTCTACTGTATTTTTC	4021	ογ
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6	GAGCCACACGGCCTCATTCTGTGAGGGAGGGAAAGATTAGCCAAAGAGTTAATTTTCAT	90	Db
3960	TGAGCCACACGGCCTCATTCTGTGAGGGAGGGAAAGATTAGCCAAAGAGTTAATTTTCAT	3901	Qy
3900	TCATCTGAAGCGTCTCTGAAATCTACCCTTGCAAGCTTCAGACAAATCAGTTGATCTCCC	3841	Db
3900	CATCTGAAGCGTCTCTGAAATCTACCCTTGCAAGCTTCAGACAAATCAGTTGATCTCCC	3841	Оу
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3840	TTCAGATTGAACAGGGATTCAGCATTCTGCCATCTCCTCATGGAAAGAGAGGCTCCC	7	ΟV
3780	GATATTTATATTTAAGTGAGTCTTAAAACCTCCTCTTATTCTACAAGTTATATGGCTA [3721	Db 49
72	TTGATCTTTTCTAATATTTTCAGAAAGTGATGGGATAACCCTAGAAGAGGACTCAGAAT	6	рь
3720	ATCTTTCTAATATTTCAGAAAGTGATGAGGATAACCCTAGAAGAGGACTCAGAAT		Qy
3660	AATTTTGGCTATTAAAGATATGTATTAGATGGTCTTATCCTGATTATTACCTGGATACAA	3601	Db
3660	TTTTGGCTATTAAAGATATGTATTAGATGGTCTTATCCTGATTATTACCTGGATACAA	3601	Qy
3600	ACCTGTGGCAGACTAGGTTTCCAGAATTTCCTGGTTCTGCTCACGTATCATGTTTGAAAA		ρb
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            Sequence 20, Application US/10121235 Publication No. US20030032609A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 358, Application US/09764864 Patent No. US20020132753A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1792
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ23
APPLICANT:
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LOCATION: (1369)
OTHER INFORMATION: n
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LOCATION: (1272)
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LOCATION: (32)
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nes 230; Conservative
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Pred. No. 1.4e-13;
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Query Match

Score 86

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; ORGANISM: Homo sapiens
US-10-121-235-20
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                                                                                                                                                                                                                                                                    Sequence 3, Application US/09852067

Patent No. US20020076777A1

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000897-CIP
CURRENT APPLICATION NUMBER: US/09/852,067
                                                                                                                                                                                           CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%;
Best Local Similarity 65.2%;
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Maemura, Koji
APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: METHODS OI
FILE REFERENCE: 05433/037001
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                                                    NAME/KEY: misc_feature
LOCATION: (1)...(31208)
OTHER INFORMATION: n =
                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                    FEATURE:
                                                                                                                                                                           LENGTH: 31208
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Windows Version 4.0
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Pred. No. 1.9e-11;
0; Mismatches 102;
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Length 31208;
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APPLICANT: HU, SONg et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001273
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09901136 Publication No. US20030039968A1
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                                                                                                                                                      239385 TAGTCTCATTAAAAATTGTACTGAGATTAATTTTAATAGTATATTTTATTCGACCCAATA 239326
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                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                           C-CCAGTAGTATACCCAAAATAGCGAAATATAGAAATTATTAATGAGATATTTTACATCC 3067
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                                                             FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                             Score 82.4; DB 9; Pred. No. 3.1e-07; 0; Mismatches 131;
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ENCODING
                                                                                                                                                                                                                                                                                                            Length 378361;
                                                                                                                                                                                                                                                                                 Indels
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; NAME/KEY: CDS
; LOCATION: 421..768
US-09-731-872-239
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Sequence 11935, Application US/09864761

Patent NO. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXTRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
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LENGTH: 1083
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Everin
TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
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SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/187,470
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Pred. No. 3
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27

APPLICATION NUMBER: GB 24263.6

APPLICATION NUMBER:

US 09/632,366

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OTHER INFORMATION: MAP TO AC021880.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.5

OTHER INFORMATION: EXPRESSED IN BADILT LIVER, SIGNAL = 0.5

OTHER INFORMATION: EXPRESSED IN ADDILT LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9-864-761-11995
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                                                                                               3087
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00661
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00670
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GTGTTCATTG-CCACATGTGGCCTGTGACTACTGTATTGGACAGTTCAG
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                                                                                             TAAATGCAGTACATATTTTATACTTACTGCATTTCTTACTTCCGAGTAGCCATATTTCAA
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                                                         AAAATCCAGTGTGCGTTTTACACTTAGAGCACATCTCAATGAGGA----CCTCATTTCAA
                                                                                                                                      ATAGCGAAATATAGAAATTATTAATGAGATATTTTACATCCTTTTTTGTACCAAGTCTTC
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Pred. No. 5.2e-08;
0; Mismatches 122;
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; LOCATION: (1)...(147399)
; OTHER INFORMATION: n - A
US-09-742-312-3
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US-09-741-149-3
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                                                                                                                                         NUMBER OF SEQ
SOFTWARE: Fast:
SEQ ID NO 3
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LI, Zhenya et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUP
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000780
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 3
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/742,312
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEC TO SEC. 2000-12-22
                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/741,149
CURRENT FILING DATE: 2000-12-21
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ORGANISM: Human
NAME/KEY: misc_feature LOCATION: (1)...(34337)
                                                FEATURE:
                                                                   ORGANISM: Human
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                                                                                                                   LENGTH:
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                                                                                                                                                                 Windows Version
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Pred. No. 8.2e-07;
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LENGTH: 13605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3446
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US-09-764-877-3446
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                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - NUMBER OF SEQ ID NOS: 4031 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
                   3038
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                                                                                                                                                                                                                                                            y Match 1.7%;
Local Similarity 55.2%;
hes 191; Conservative
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                                                                                                                       GAGCCACATGTATAACTTCAATTGTCTAGTTAGCCTCATTAGGAAAAGCAAAAATAACTT 3143
                                                                                                                                         AAGTCACATATTTTATTTAAAAATTTTCTAGTAACATAAACAAAGTAAAAGTGA--G 2977
                                                                                                                                                                                          ACACTACTGCTTATCCATCTCTTATTTCTAGACCAGCACTGTCCTATAGAAAT---ATGT 3083
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                                                                                   CAGGGCAAAATAATTTTGATATTACTTTTCACCCAGTAGTATACCCAAAATAGCGAAATA 3037
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                                                                                                                                                                                                                                                            Score 76; DB 10; Pred. No. 1.6e-06; 0; Mismatches 150;
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US-10-229-124-3
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                                                                           Sequence 1, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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Publication No. US20030013168A1
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Best Local Similarity
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TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN I
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001139DIV
CURRENT APPLICATION NUMBER: US/10/229,124
CURRENT FILING DATE: 2002-08-28
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Marti
APPLICANT: Parker, Alexande
TITLE OF INVENTION: METHODS
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                   Barrington-Martin,
Parker, Alexander
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  AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC
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Pred. No. 6.3e-06;
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US-09-736-960-86/c
: Sequence 86, Application US/09736960
: Patent No. US20020102267A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Candia III, Albert Frederick APPLICANT: Arbor Vita Corporation TITLE OF INVENTION: CLASP-5 Transmembrane FILE REFERENCE: 020054-000511US CURRENT APPLICATION NUMBER: US/09/736,960 CURRENT FILING DATE: 2001-09-20
                                                                                         PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR FILING DATE: 2000-04-11
                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/547,276 PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/160,860 PRIOR FILING DATE: 1999-10-21 PRIOR APPLICATION NUMBER: US 60/162,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA FILE REFERENCE: 3322/11702 USCHIZOPHRENIA CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/170,453 PRIOR FILING DATE: 1999-12-13
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                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-10-29
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                                               FILING DATE:
                                                                     APPLICATION NUMBER: US 60/196,460
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Candia III, Albert Frederick
Arbor Vita Corporation
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Pred. No. 1.4e-05;
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US-09-822-246-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: ordered human genomic DNA at CLASP-5 locus US-09-736-960-86
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUP
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001149
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09822246 Patent No. US20020142383A1
                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/822,246 CURRENT FILING DATE: 2001-04-02
                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,508
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,539
PRIOR FILING DATE: 2000-10-13
                                                                  TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,503
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NAME/KEY: misc_feature LOCATION: (1)...(197997)
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                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Local Similarity 59.7%;
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APPLICATION NUMBER: US 60/196,528
FILING DATE: 2000-04-11
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                                                                                                                                                                                                                                                                                         ENCODING HUMAN TRANSPORTER PROTEINS
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; OTHER INFORMATION: n = A,T,C US-09-822-246-3

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1297
; LENGTH: 12047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1297
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US-09-764-847-1297
Sequence 1297, Application US/09764847
Patent No. US20020132767A1
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
                                                                                                                                                                                                                                                                                                               Query Match 1.5%; Score 70; DB 10; Length 12047; Best Local Similarity 59.2%; Pred. No. 3.2e-05; Matches 174; Conservative 0; Mismatches 115; Indels 5
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Best Local :
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
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3087 TAAATGCAGTACATATTTTATACTTACTGCATTTCTTACTTCCGAGTAGCCATATTTCAA 3146
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Local Similarity 56.4%;
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                                                                                                                                              AAACAGATGAAATTAGTAATATTTTTAAAATCCAGTATATCCCAAGTATGGTTATTTT 1470
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                                                                                    ATAGCGAAATATAGAAATTATTAATGAGATATTTTACATCCTTTTTTTGTACCAAGTCTTC 3086
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                                                              AGCATGTAATCAATATA-AAATAATAAGATATTTTACATTCTTTTTT---TCTAGTCTTT 1526
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Pred. No. 7.3e-05;
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Db 1527 GAAATTTGGTGCATATTTTACACTTATGGCACATCTCAATTCAGACTATCCACATTTCAA 1586
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Search completed: March 22, 2003, 14:37:45
Job time: 2155 secs

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Minimum DB seq
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Perfect score:
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Maximum Match 10
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934.6
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312
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1: /cgn2_6/ptodata/2/pna/U
2: /cgn2_6/ptodata/2/pna/U
3: /cgn2_6/ptodata/2/pna/U
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6: /cgn2_6/ptodata/2/pna/U
8: /cgn2_6/ptodata/2/pna/U
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length: 2000000000
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4526
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO7_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USIO_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/USIO_NEW_COMB.seq:*
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                   first 45 summaries
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US-10-342-887-77
US-10-144-771-15372
US-09-912-293-92043
US-09-912-293-91554
US-09-912-293-91514
US-09-912-293-911-36747
US-09-912-293-18131
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US-09-947-911-240
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Compugen Ltd
 Sequence 77, Appl Sequence 15372, A Sequence 92043, A Sequence 9911, A Sequence 96911, A Sequence 15516, A Sequence 15516, A Sequence 15516, A Sequence 24291, A Sequence 218131, A Sequence 1729, Ap Sequence 2720, Ap Sequence 270, App Sequence 803, App Sequence 803, App Sequence 803, App Sequence 469, App Sequence 469, App Sequence 682, App Sequence 682, App Sequence 682, Appli Sequence 8, Appli Sequence 55, Appli Sequence 55, Appli Sequence 55, Appli
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RESULT 1 US-10-342-887-77 Sequence 77, A GENERAL INFORM APPLICANT: DA APPLICANT: H APPLICANT: H APPLICANT: M		c 45	C 44	4	c 42				38	37		c 35		33	32	31	c 30		28	27	c 26		
SULT 1 -10-342-887-77 -10-342-887-77 Sequence 77, Applica GENERAL INFORMATION: APPLICANT: Dai, Hor APPLICANT: Linsly APPLICANT: Linsly APPLICANT: Mao, Ma		77.8	77.8	78.4	78.8	79		•	79.4	79.4	79.4	•	80.6	۲.			83.6	84.2	85	86.2	86.8	87	
SULT 1 -10-342-887-77 -10-342-887-77 Sequence 77, Application US/10342887 GENERAL INFORMATION: APPLICANT: Dai, Hongyue APPLICANT: Linsley, Peter S. APPLICANT: Mao, Mao	ALIGNMENTS	1.7 2605602 5 US-09-947-911-314	9	6		6	5 U	20 5	72178 6	œ б _	.8 601 6	.8 145	.8 601 6	366 6	.8 13712 8 U	в 5	5 U	5			1.9 31208 8 US-10-338-691-3	596	
		Sequence 314, App	243, Ap	13634,	1148,	608,		e 49,	471,	691,		7, Ap		117056	1504	26	14, 2	86,	e 54,	327	껉	Sequence 1022, Ap	

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TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-77
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APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR PILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                            Query Match 88.7%;
Best Local Similarity 98.7%;
Matches 4080; Conservative
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TGCCAAGGTTAATTGTGTCAAAGAAGAAATATCAAGATACTGTGGAAAAGAAAAGGATTT
                                               ----TCTTGAAGAACTGAATGAGGCTGTTAGACCTCTGCAGGACTATGGAATTTCAGT
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ACAGGCTACTTATGAAGCTGATAGAAGAACTGCAGAATGGGTTGCTTGGCGTCTTCTGGG
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CATTCACCTGTTTATTAAGACAATGAAAGCACCTCTGTTGACTGAAGTTGCTGAAGATCC
CTTGGACTTGACCCAGCAATGTAGAAGAACACTAATGGAACAGCCATTGACTACACTGAA
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          ATTTTCAGAAAGTGATGGGATAACCCTAGAAGAGGACTCAGAATGATATTTATATTTTAA
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TGAAATCTACCCTTGCAAGCTTCAGACAAATCAGTTGATCTCCCTGAGCCACACGGCCTC
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503	434	452	392	ery M st Lo tches	TYPE: DNA ORGANISM: 10-144-771	OMBER CO ID I	URREN	TTLE (JLT 2 0-144 equence	4081	4457	4397		4337	3901	4277	84	ა -	4157	3721	4097	3661	4037	3601	3977	3541	3917	3481
TCTTGAAGAACTGAA 517	TCTCTCCCAGAACTGACTCCTCA	GTCCTCAGAAATATTTTAGTACATTGCAA	TGTCTTTAGAGTTGGGATCTCTTTTGTCATAATGTGCATTTTTTACATGCCACACAGTAAA 451 	ch 20.6%; Score 934.6; DB 8; Length 3756; 1 Similarity 63.7%; Pred. No. 2.5e-186; 1 Similarity 63.7%; Pred. No. 2.5e-186; 1 Indels 446; Gaps	DNA SM: HUMAN 771-15372	OF SEQ ID NOS: 47235 to 15372 to 3756	PERKENE: CLUUI321 PAPPLICATION NUMBER: US/10/144,771 PILING DATE: 2002-05-15	NT: VENTER, J. Craig PINCENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF	US-10-144-771-15372 ; Sequence 15372, Application US/10144771 ; GENERAL INFORMATION:	GTCATTAATGTTTGTCATAATTTTAAATAAAGTGTCTGGGTTTCAGAATACCTTC 4135	GTCATTAATGTTTGTCATAATTTTAAATAAAGTGTCTGGGTTTCAGAATACCTTC 4511	TACCAGCACATAGAAACATGAAATTGCTTAGTCATTGTACCTTTGTCAGCAATTTTGACA 4456	aaatataggttgtagtaataaaacatcattagcctaattattagaaaatgctaattaag 402	TAAATATAGGTTGTAGTAAAAACATCATTAGCCTAATTAGAAAATGCTAATTAAG 4396	CTGATTAAACTCATTTTCATTTTGCTTTTATTTCTAATATGGGAACAATGAGAGTGAACTC 3960	- 14	CCGTTGCTACTCTCAGCACCCTCTCCTCAATTTTTTTCCTGTAGCATGTGATGC 390	1977 - O'GERACHEONERCHANDA EN GEOLOGICO DE CONTROLOGICO DE	ACTGAAATTTAAGGAATCTAACAGCTAAAACTCAGTAAGTGCATMTATTTCCTTATAACA 4216	GATATCTTGTTCTTTAAATTTTCTTCACATATGGTTTGCCTGATACAACTGATTTTTATA 3780	GATATCTTGTTCTTTAAATTTTCTTCACATATGGTTTGCCTGATACAACTGATTTTTATA 4156	ACATTTGTTGAGAATATTCTATTTGGTGCTCTACTGTATTTTTTTT	ACATTTGTTGAGAATATTCTATTTGGTGCTCTACTGTATTTTTCTTTTTAATATCTACTT 4096	GTTAGACTGATCTGTTTGTAGCAGTTGTTTGTCTCATTTTTGCTCTGTGCATTTTTTGAG 3660	TTAGAC	360	ATTCTGTGAGGGAGGGAAAGATTAGCCAAAGAGTTAATTTTCATTCCAAATCACTTAGCT 3976	

.597	8 GGCTTCTGACAGCATAGTACTCTTCTATGCTGGTTGGCAAGCAGTATCCATGGCATTTTT 1	153	Qy
.345	6 ACCACTACCTTTGGAGTTGTCTGTGGAGCTAACAGAGGAGACTTTTAATACAACGGTC	128	Db
537	8 AAAATTACCTTTGGAACTTACAGTGGAACTAACAGAAGAAGAACATTTAATGCAACAG	147	Qy
.285		122	рь
.477	8 TCCAGATATAGATGTTCAGGATGATGAAGTGGCAGAAACTGTTTTCAGAGATAGGAAG	141	Qy
N	6 CGTGAAAAATAATATGCACATTGAAGAAATACAAGAAGATGAAGGCGAAGACATGGAGGG	<u> </u>	Db
417	8 TGTGGAAAATAATATGCACATTGAGGAAATACAAGAAGATGAAGACAATGACATGC	135	γO
165	2GATGTGCCTGTGGAGTTTCTGGTGTTGAATGATGTTGAGTTAATCA	111	DЬ
357	8 AGAAGAGGGAGTTCCAGTGGAATTTTTGGTATTACATGATGTTGATTTAATAATATCTC	129	Qy
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.297	8 GTTAAGGGACTCTTTGGAAGTGAACATTCCTCAAGATGCTAATGTGGTCTTCAAAAGAGC 1	123	Qγ
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237	8 TAGAAGAACTGCAGAATGGGTTGCTTGGCGTCTTCTGGGAAAAGCAGGAGTTCTACTCTT 1	117	Qy
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177	TTTATTGT	111	Qy
[111	AATGAACGCACCTCTGTT1	109	Db
1117	8 AATGAAAGCACCTCTGTTGAC	105	Qy
1093	4 CAGAAGAACACTAATGGAACAGCCATTGACCACTCAATATTCACGTATTTGTGAAGA	103	В
1057	8 TAGAAGAACACTAATGGAACAGCCATTGACTACACTGAACATTCACCTGTTTATT	99	Qy
1033	4 AGAACATGCACATCTCTACTTTTTCATTGTAAACTGGTCTTGGACTTGACCGAGC	97	дb
)97	8 GGAATATGCACATCTCTACTTTTTCATTGTAAACTAGTCTTGGACTTGACCC	93	Qy
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337	8 ATACCAATTIGICTTAACCACAGAAATIGCCCTTTIGGAAAGTATIGGCTCIGAGGA	87	Qy
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537	8 AGAAGAAATATCAAGATACTGTGGAAAAGAAAAGGATTTGATGAAAGCATATTTATT	57	Qy
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GATAAATCGGC 267 	TGTATGAAAGAAACAGATGTGCAGGAGAATGATAAGGA 	ω		
AAAGTTCCCAA AAAGTTCTAGA	TGATTTTCTAAGTATGATAGATGCCGCAACATCTCAACGTGGCACTAGGAAAGTTCTAGTTTCTGATTTCTGATTTCTGATGGACGCTCCTACATCCCAAGCTCCCACGAAGAAAGTTC	558 276	Qу 2 Db 2	
CTCTTCCAGCTTA 2	ACTAGAAAATCATATCACAATTTTACCTGCTCAAGAATGGAAACCTCCT	498 216	Qy 2 Db 2	
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CCTCAATATAA GCTGGTTAAAT	CAGACTTCAGAAACCATTATTGATTTTGTTCAGTGATGGCACTGTAAATCCTCAATA	198	Db 1	
GTACAGGA	AAATGCACTACTGGAAGCATTTTGGTGGCAGCA	88		
CCCAGTTATTT	AACAGATGCACTACTGGAAATGTTTCCGGAAAATCACTGTGGAAAATCTTCCCA	138	Qy 2	
GCTCAGATACT	AGGTAGAATAGAGAGTGTCCCACTAGACACCCTGGTACAAGACATGGCTCAGAT	82		
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ACAG	GCTACTGTCAACCAAATATGCTGCAAGTCTTCCAGCCCTGCTGCTTGCCAGACAC	01		
	AGCAGGAAAGCAGCTGAGAGGCTCTGTCATTACGGGAATTTATTCTGAAGATGATGT	706	Db 1	
AGAAGATGTTTT	CCTAAAAGGATATGTTATC	958	Qy 1	
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GATTTTAGI	TGTGTCAGTATTGGGACTATTTAGTCCAACCATGAAAACAGCAAA	89		
CATCTTGTATTCTAG 	CCAAGAAGCAGAAAAATATTTAAGTGGGGAATTATATAAAGCCT	586	Db 1	
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ATAACATC	AGATCTCCTAAAATTTATCCAGCTCAACAGGATTTCATATCCAGTGAAI	77	Qy 1	
TTGGCAACTAA	GGTAAAGTTGTAT	466	Db 1	
STTAGGAACCAA	CATAAAGATGTACAAGAAAGGCGAGAACCCCAGTATCTTATGCTGGAATGTTAGGAACC	718	Qy 1	
TACTGCATTTCCCGT	AATAAATTGTGCAGATTGGTCTGATATATGTACGAAGCAAAATGT	406	Db 1	
- <u>C</u>	AATAAACTGTGCAGATTGGTCTGATGTATGTACTAAGCAAAATGT	.658	Qy 1	
CTTCTCACCAG		381	Db 1	
TTACT	GCAATCCTATATTGATGTGGCAGTTAAACTG	.598	Qy 1	
	GACTTCTGACAGCATAGTGCTCTTCTATGCTACCT	.346	Db 1	

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US-09-912-293-92043
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                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 09/249,651
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
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CURRENT FILING DATE: 2001-07-26
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PRIOR APPLICATION NUMBER: 09/813,155
PRIOR FILING DATE: 2001-03-21
Remaining Prior Application data rem
NUMBER OF SEQ ID NOS: 244538
                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PO-100
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OR APPLICATION NUMBER: 08/221,623
OR FILING DATE: 1994-03-31
OR APPLICATION NUMBER: 08/220,691
OR FILING DATE: 1994-03-31
OR APPLICATION NUMBER: 09/741,830
                                                                                                                                                           APPLICATION NUMBER: 09/859,490 FILING DATE: 2001-05-18 APPLICATION NUMBER: 08/196,362
                                                         FILING DATE: 2000-12-22
                                                                                                                                                                                                         FILING DATE: 1994-02-15
                                                                                                                                                                                                                       APPLICATION NUMBER: 08/196,363
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; LOCATION: (433)..(433)
; OTHER INFORMATION: n is
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                                            Query Match
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; NAME/KEY: misc_feature
; LOCATION: 333
; OTHER INFORMATION: w-a
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Best Local Similarity
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SEQ ID NO 32911
LENGTH: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-02-26
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                                                                                                                    LOCATION: 326
OTHER INFORMATION: n-a,
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Query Match
Best Local Similarity
Matches 312; Conserv
                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 244538 SEQ ID NO 91554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 91554, Application US/09912293 GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/912, 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/103,744 PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
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                                                                                                                                                FEATURE:
                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/
FILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/196,362 FILING DATE: 1994-02-15 APPLICATION NUMBER: 08/221,623
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/859,490 FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1993-08-09
APPLICATION NUMBER: 08/196,363
FILING DATE: 1994-02-15
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/741,830
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/813,155
                                                                                                                                                                                                                                                                                                    FILING DATE:
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99.7%;
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        Score 312; DB 6;
Pred. No. 6.7e-56;
0; Mismatches 1
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1911 GGACTATTTAGTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAGGAAACTAC 1970

ture	s equal to a,t,q, or	; FEATURE: ; NAME/KEY: mlsc_feature ; LOCATION: (150)(160) ; OTHER INFORMATION: n is equal to a,t,g, or c	misc_ (10). ORMATI	96911 496 . Homo sapien	APPLICATION N FILING DATE: ning Prior App R OF SEQ ID NO	APPLICATION N FILING DATE: APPLICATION N FILING DATE:	APPLICATION N FILING DATE: APPLICATION N FILING DATE:	APPLICATION NUMBER: 0 FILING DATE: 1994-02- APPLICATION NUMBER: 0 FILING DATE: 2001-05-	APPLICATION NUMBER: 0 FILING DATE: 1999-02- APPLICATION NUMBER: 0 FILING DATE: 1993-08-		INFORMATION: NT: Rosen, et. al. FINVENTION: Human G FERENCE: PO-100	RESULT 6 US-09-912-293-96911 ; Sequence 96911, Application US/09912293	Qy 2211 CCATTATTGATTT 2223	Qy 2151 CTGGAAATGTTTCCGGAAATCACTGTGGAAAATCTTCCCCAGTTATTTCAGACTTCAGAAA 2210	QY 2091 AGCATCCCACTAGCTAGCACACACACGCACAAGACATAGTTCAAATAATAACAGATGCACTA 2150	QY 2031 AAATATGCTGCAAGTCTTCCAGCCCTGCTGCTTGCCAGACACAGAAGGCAAAATAGAG 2090	Qy 1971 CTAAAAGGATATGTTATCACTGGAATTTATTCTGAAGAAGATGTTTTGCTACTGTCAACC 2030	Db 1 GGACTATTTAGTCCAACCATGAAAACAGCAAAAGAAGATTTTAGTGAAGCAGGAAACTAC 60
; NAME/KEY: misc_feature ; LOCATION: (481)(481)	NAME/KEY: misc_feature LOCATION: (472). (472) OTHER INFORMATION: n is equal to a,t,g, or c FEATURE:	; NAME/KEY: misc_feature ; LOCATION: (445)(445) ; OTHER INFORMATION: n is equal to a,t,g, or c ; FEATURE:	글 ~ 급 >	; NAME/KEY: misc_feature ; LOCATION: (439)(439) ; OTHER INFORMATION: n is equal to a,t,g, or c ; FEATURE:	; NAME/KEY: misc_feature ; LOCATION: (426)(426) ; OTHER INFORMATION: n is equal to a,t,g, or c ; FEATURE:	NAME/KEY: misc_feature : LOCATION: (420)(420) : OTHER INFORMATION: n is equal to a,t,g, or c : FEATURE:	NAME/KEY: misc_feature ; LOCATION: (411)(411) ; CHER INFORMATION: n is equal to a,t,g, or c FEATURE.	NAME/KEY: misc_feature; LOCATION: (407)(407) OTHER INFORMATION: n is equal to a,t,g, or c FEATURE:	NAME/KEY: misc_feature; LOCATION: (404)(404) OTHER INFORMATION: n is equal to a,t,g, or c FEATURE:	NAME/KEY: misc_feature; LOCATION: (367)(367) OTHER INFORMATION: n is equal to a,t,g, or c FEATURE:	NAME/KEY: misc_feature ; NAME/KEY: misc_feature ; LOCATION: (353)(353) ; OTHER INFORMATION: n is equal to a,t,g, or c ; FRATURE:	NAME/KEY: misc_feature COCATION: (347)(347) COTHER INFORMATION: n is equal to a,t,g, or c FEATURE:	NAME/KEY: misc_feature ; NAME/KEY: misc_feature ; LOCATION: (332)(333) ; CTHER INFORMATION: n is equal to a,t,g, or c FEATURE.	D H X :		NAME/KEY: misc_feature ; NAME/KEY: misc_feature ; LOCATION: (238)(238) ; OTHER INFORMATION: n is equal to a,t,g, or c FRATURE:		; LOCATION: (214)(214) ; OTHER INFORMATION: n is equal to a,t,g, or c

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CURRENT APPLICATION NUMBER: US/10/349,781
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 09/540,764
PRIOR FILING DATE: 2000-03-30
PRIOR PRIOR APPLICATION NUMBER: 08/992,868
PRIOR APPLICATION NUMBER: 08/932,838
PRIOR APPLICATION NUMBER: 60/032,838
PRIOR APPLICATION NUMBER: 08/734,050
PRIOR APPLICATION NUMBER: 08/734,050
PRIOR FILING DATE: 1996-10-18
PRIOR PILING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: 60/006,111
PRIOR FILING DATE: 1995-10-24
PRIOR PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: 60/005,864
PRIOR APPLICATION NUMBER: 60/005,864
PRIOR APPLICATION NUMBER: 60/005,864
PRIOR APPLICATION NUMBER: 09/763,920
PRIOR APPLICATION NUMBER: 09/763,920
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US-09-912-293-96911
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Best Local
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo APPLICANT: Stuart, Susan G.; Stuve, Laura L. APPLICANT: Mullahy, Sara J.; Naughton, Rebecca E. TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TIS FILE REFERENCE: PD-1028-2 CON
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DR APPLICATION NUMBER: 60/005,864
DR FILING DATE: 1995-10-26
DR APPLICATION NUMBER: 08/763,920
DR FILING DATE: 1996-12-11
DR APPLICATION NUMBER: 60/008,794
DR FILING DATE: 1995-12-14
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Pred. No. 3.6e
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B.6e-46;
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US-10-349-781-36747
; Sequence 36747, Application US/10349781
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1996-12-23
Remaining Prior Application dat
NUMBER OF SEQ ID NOS: 61458
SOFTWARE: PERL Program
SEQ ID NO 15516
LENGTH: 257
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local 9
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                                           PRIOR FILING DATE: 1996-12-11
PRIOR APPLICATION NUMBER: 60/008,794
PRIOR FILING DATE: 1995-12-14
PRIOR APPLICATION NUMBER: 08/772,783
PRIOR FILING DATE: 1996-12-23
PRIOR FILING DATE: 1996-12-23
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PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/032,838
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: 08/734,050
DELIG ETITAL 1066-12-13
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/349,781
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 09/540,764
PRIOR FILING DATE: 2000-03-30
 Remaining Prior Application data
NUMBER OF SEQ ID NOS: 61458
SOFTWARE: PERL Program
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nes 257; Conserv
                                                                                                              APPLICATION NUMBER: 60/005,864 FILING DATE: 1995-10-26 APPLICATION NUMBER: 08/763,920 FILING DATE: 1996-12-11
                                                                                                                                                                                  APPLICATION NUMBER: 08/733,814 FILING DATE: 1996-10-18
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APPLICATION NUMBER: 60/006,111
FILING DATE: 1995-10-24
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Wrapper or PALM

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APPLICANT: Seilhamer, Jeffrey J.; Delegeane, APPLICANT: Stuart, Susan G.; Stuve, Laura L. APPLICANT: Mullahy, Sara J.; Naughton, Rebertitle Of INVENTION: POLYNUCLEOTIDES OF CELLS FILE REFERENCE: PD-1028-2 CON
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; OTHER INFORMATION: Incyte
US-10-349-781-36747
               SEQ ID NO 24291
LENGTH: 228
TYPE: DNA
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                                                                    Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 61458 SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/349,781
CURRENT FILING DATE: 2003-01-21
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 245
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                                                                                                                                                                  FILING DATE: 1995-12-14
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APPLICATION NUMBER: 08/733,814
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Pred. No. 7.3e-42;
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CELLS AND TISSUES
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US-09-912-293-18131; April 18131; 
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; OTHER INFORMATION: Incyte ID No: hu00693953
US-10-349-781-24291
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PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
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CURRENT FILING DATE: 2001-07-26
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PRIOR APPLICATION NUMBER: 08/221,623
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NAME/KEY: misc_feature LOCATION: (223)..(223) OTHER INFORMATION: n is
                                                                                                                                      NAME/KEY: misc_feature LOCATION: (201)..(201) OTHER INFORMATION: n i:
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LOCATION: (172)...(172)
OTHER INFORMATION: n is
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Pred. No. 2.6e-38;
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FEATURE:

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RESULT 11
US-09-539-806B-30366
US-09-539-806B-30366, Application US/09539806B
; GENERAL INFORMATION:
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                         APPLICANT:
APPLICANT:
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Best Local Similarity
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                                                               BENERAL INFURMATION.
APPLICANT: Seilhamer, Jeffrey J.
                                                  APPLICANT:
TITLE OF INVENTION:
                APPLICANT:
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LOCATION: (239)..(239)
OTHER_INFORMATION: n is
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LOCATION: (304)..(304)
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LOCATION: (275)...(275)
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                        Stuart, Susan G.
Stuve, Laura L.
Mullahy, Sara J.
                                                  Delegeane, Angelo
Stuart, Susan G.
 Naughton, Rebecca E. POLYNUCLEOTIDES
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Pred. No. 5.3e-30;
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Sequence 1729, Application US/10349781

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.; Delegeane, An APPLICANT: Stuart, Susan G.; Stuve, Laura L. APPLICANT: Mullahy, Sara J.; Naughton, Rebecca TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AN FILE REFERENCE: PD-1028-2 CON CURRENT APPLICATION NUMBER: US/10/349,781

CURRENT FILING DATE: 2003-01-21
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SEQ ID NO 30366
LENGTH: 181
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Best Local Similarity
                                 PRIOR APPLICATION NUMBER: 09/540,764
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/992,868
PRIOR FILING DATE: 1997-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/016, PRIOR FILING DATE: April 18, 1996 PRIOR FILING DATE: Application data and the prior Application data NUMBER OF SEO ID NOS: 48372
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PRIOR APPLICATION NUMBER: 60/004,676
PRIOR FILING DATE: October 2, 1995
PRIOR APPLICATION NUMBER: 08/749,515
PRIOR APPLICATION NUMBER: 15, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PD-1027
CURRENT APPLICATION NUMBER
CURRENT FILING DATE: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: November PRIOR APPLICATION NUMBER: 6
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FILING DATE: March 20, 1996
APPLICATION NUMBER: 08/951,197
FILING DATE: October 1, 1997
APPLICATION NUMBER: 60/027,249
FILING DATE: October 1, 1996
APPLICATION NUMBER: FILING DATE: 1996-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/006,810 FILING DATE: November 15, 1995
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APPLICATION NUMBER: 08/826,438
FILING DATE: March 20, 1997
APPLICATION NUMBER: 60/016,145
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Pred. No. 1.8e
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1.8e-28;
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RESULT 13
US-10-349-781-23200
US-10-349-781-23200, Application US/10349781;
GENERAL INFORMATION:
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; OTHER INFORMATION: Incyte ID No: hu00878731
US-10-349-781-1729
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                                                                                   PRIOR APPLICATION NUMBER: 09/540,764
PRIOR FILLING DATE: 2000-03-30
PRIOR PELICATION NUMBER: 08/992,868
PRIOR FILLING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/032,838
PRIOR FILLING DATE: 1996-12-13
PRIOR PELICATION NUMBER: 60/734,050
PRIOR FILLING DATE: 1996-10-18
PRIOR FILLING DATE: 1996-10-18
PRIOR FILLING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: 60/006,111
PRIOR FILLING DATE: 1995-10-24
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PRIOR FILING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: 60/005,864
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: 08/763,920
PRIOR APPLICATION NUMBER: 60/008,794
PRIOR APPLICATION NUMBER: 60/008,794
PRIOR FILING DATE: 1995-12-14
PRIOR PRIOR FILING DATE: 1995-12-14
PRIOR FILING DATE: 1996-12-23
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                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/349,781 CURRENT FILING DATE: 2003-01-21
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ORGANISM: Homo sapiens
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FILING DATE: 1996-10-18
APPLICATION NUMBER: 60/005,864
FILING DATE: 1995-10-26
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                                                                 APPLICATION NUMBER: 08/733,814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTTCTTTTTAGTGAAGTGAAATATATTACCAACCTGGAAGACCTTCAGAACATAGAAA 774
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190; Conserv
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Pred. No. 4.9e-28;
0; Mismatches 0
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; OTHER INFORMATION: n = A,T,C
US-09-947-911-240
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US-09-947-911-240/c
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Best Local S
Matches 253
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 240
LENGTH: 1043426
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LENGTH: 176
                                                    847450 TAAAAACATGGTATAGCTTTTAAATGATTTGGAATGGTGCTATTTAATAGAAATATATTA 847391
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PRIOR APPLICATION NUMBER: 60/008,794
PRIOR FILING DATE: 1995-12-14
PRIOR APPLICATION NUMBER: 08/772,783
PRIOR FILING DATE: 1996-12-23
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NUMBER OF SEQ ID NOS: 368
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SOFTWARE: PERL Program
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                                                                                                                                                                                              Match 2.4%;
Local Similarity 60.0%;
nes 253; Conservative
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TAAGTCACATATTTTATTTAAAATTTTCTAGTAACTACATTAAACAAAGGTAAAAGTGAGC 2978
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                                                                       AAGAATAATATTAAATCATTTCAAGTTTGCAGACTAGTGCCATCCAATAGAATTATAATA 2918
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                                                                                                                                                                                              Score 108.4; DB 5;
Pred. No. 1:4e-12;
0; Mismatches 161;
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US-09-949-002-578
Sequence 578, Application US/09949002
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION UMBER: US/09/949,002
CURRENT ETLING DATE: 2000-01-28
CURRENT FILING DATE: 2000-01-28
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US-09-949-002-578
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 578
LENGTH: 76321
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PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF THE PRIOR P
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43202 AGTGGCTACCATATTGAACAATGCAGTTATAGACCA 43237
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Search completed: March 22, 2003, 14:25:08 Job time : 2606 secs

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Result
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BF458491 UI-M-BZI-	F	BM9414/8 UI-M-BZ1-	BQ215516 AGENCOURT	AA737677 nw63b12.s	AI333002 qq18g07.x	AA773166 ab66a02.s	BI689253 603316575	BI655128 603280926	AI140821 oo15d01.x	BQ919809 AGENCOURT	AW150811 xg39e10.x	H06836 yl83g09.rl	AA113931 zn27d09.s	AI014524 ou32g09.x	AI453818 tj29d02.x	AI306463 qn13a04.x	AW131649 xf32f11.x	AA278675 zs77d04.s	AI832055 wj99g05.x	BI689134 603315939	AI333000 qq18g05.x	BG609542 323429 MA	AA278257 zs77d04.r	AA113856 zn27d09.r	BI712755 ie08h05.y	BG863191 602796673	AA934775 om78f08.s	AW131594 xf31h02.x	AV662311 AV662311	AW665394 hi90c01.x	BF790996 602251048	- BE895218 601433654	AL040840 DKFZp434F	BM972493 UI-CF-EC1	BG928131 HNC65-1-B	EST373	BI712516 ie08h05.x	AV6461

ALIGNMENTS

JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1 AU124110 LOCUS SOURCE ORGANISM DEFINITION TITLE AU124110 AU124110.1 HRI human CDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3985 Isogai,T. HRI human Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 784)
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and AU124110 AU124110 EST Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Homo sapiens human. sequence NT2RM2 Homo sapiens GI:10948826 784 bp mRNA linear EST 01-AUG-2002 cDNA clone NT2RM2001681 5', mRNA

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BASE COUNT
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/db_xref="taxon:9606"
/clone="NT2RM2001681"
/clone=lib="NT2RM2"
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precursor cells"
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/cell_line="NT2"
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Tissue Procurement: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg,
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National Institutes of Health, Mammalian
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UI-E-EO1-aiv-d-13-0-UI.rl UI-E-EO1 Homo sapiens cDNA
UI-E-EO1-aiv-d-13-0-UI 5', mRNA sequence.
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                             451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                       Program for Rat Gene Discovery and Mapping University of Iowa
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TATGTATTAGATGGTCTTATCCTGATTATTACCTGGATACAACTTGATCTTTTCTAATAT 3678
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                                                                                                                                                                                                                                                                                                                                                                 TATTTCAAGTGTTCATTGCCACATGTGGCCTGTGACTACTGTATTGGACAGTTCAGTACT 3198
                                                             TTCCAGAATTTCCTGGTTCTGCTCACGTATCATGTTTGAAAAAATTTTTGGCTATTAAAGA 3618
                                                                                                                                           ATGGTAGTCGTGCCAAGGCTGAGTAACCTTGTGTTAAAAGTAACCTGTGGCAGACTAGGT 3558
                                                                                                                                                                                                        GATCCTGCTAAATAACCTGCATTGGACAGCGCCCCCACAACAAAGAATTATCCTGCCCGAA
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                                        TTCCAGAATTTCCTGGTTCTGCTCACGTATCATGTTTGAAAAAATTTTGGCTATTAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           >MER20#DNA/MER1_type
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Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-off primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonuclectide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."

21 a 137 c 143 g 250 t 2 others
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/dev_stage="fetal"
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/db_xref="taxon:9606"
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Pred. No. 1.3e-124;
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                         AGAATTATCCTGCCCGAAATGGTAGTCGTGCCAAGGCTGAGTAACCTTGTGTTAAAAGTA 3540
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AGAATTATCCTGCCCGAAATGGTAGTCGTGCCAAGGCTGAGTAACCTTGTGTTAAAAGTA
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AU119721
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HRI human cDNA project; 5'- & 3'-end one pass sequenci
Research Institute; cDNA library construction: Departm
Virology, Institute of Medical Science, University of
Helix Research Institute.
Location/Qualifiers
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1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
Fax: 81-438-52-986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Takao Isog:
Genomics Laboratory
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1 (bases 1 to 743)
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1006479"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mai/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
a 141 c 147 g 254 t
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Sugano,S. an
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inowe,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra s
                                                                                                                                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                     AK017582

AK017582.1 GI:12856892

HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 8 days

clone_lib:RIKEN full-length enriched m
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730420B22:homolog to KIAA1344 PROTEIN (FRAGMENT), full insert sequence.

AK017582
                                                                                                                                                                                                                                                      Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Eutheria;
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Rodentia;
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Sciurognathi;
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nouse cDNA library
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
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Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
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Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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5 (bases 1 to 1266)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details.
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                               /organism="Mus musculus"
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AGTCATGGAAGCTGCTTTTGTGTATGGGACCTCTTACCAGTTTGCCTTAACCACAGAAAT
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/db_xref="GI:12856893"
/db_xref="MGD:MGI:1917811"
/translation="MMSSGFSVFRAGVALVLMCSFYKSTEDSLPELTPQQYFSTLQPG
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/dev_stage="8 days embryo"
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to KIAA1344 PROTEIN (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM12761 row: c column:
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National Institutes of Health, Mammalian
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BM552780
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                                                                                                                                                                                                                                                 quality sequence stop: 628
                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5742650"
/clone_llb="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV Site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for
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RESULT 7 AV646118 LOCUS

KEYWORDS SOURCE

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GLC Homo sapiens

605 605 bp

clone

mRNA linear ne GLCAJF06 3',

EST 15-JAN-2002 mRNA sequence.

'n

GI:9867132

REFERENCE

AUTHORS

TITLE

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X. Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Sl
201203, p. R. China
Tel: 86-21-50801919 (ex.45)
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clone is available at CHGC
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/dev_stage="Adult"
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/db_xref="taxon:9606"
/clone="GLCAJF06"
/clone_lib="GLC"
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  4096 TGATATCTTGTTCTTTAAATTTTCTTCACATATGGTTTGCCTGATACAACTGATTTTTAT 4155
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information
Washington University Genome Sequencing Center For information
Washington University Genome Sequencing Center For Inoue
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Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
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Fax: 617-495-8557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Seq primer: -40UP from Gibco
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noti; Site_2: Nhol; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div (Alan Permutt Lab), Mashington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, Mo 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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/db_xref="taxon:9606"
/clone="IMAGE:5086689"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Contact: John Quackenbush
The Institute for Genomic Research
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/db_xref="taxon:9606"
/db_mref="MAGE resequences,
/note="Vector: pBluescriptSKm"
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GlaxoSmithKline 709 Swedeland Road, Tel: 610-270-7245 sequenced tags (ESTs) each from adult human osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001) Fax: 610-270-5598 Email: sanjay_kum Osteoarthr. Cartil. 9 21482651 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; EST UW2109 Contact: Sanjay Kumar Identification and initial characterization Homo sapiens Lark, M.W (bases 1 to 686) sanjay_kumar-l@gsk.com /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HNC (Human N Location/Qualifiers
1. .686 ש . ! Box 1539, Normal King Cartilage)" of Prussia, normal and of 5000 expressed PA 19406, Euteleostomi; Gowen, M. Mao, USA

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                                                                                         Eukaryota;
Mammalia; E
                                                                                                              Homo sapiens
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                 Contact: McCray, PB
                              97044477
                                      Genome Res. 6 (9),
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University of Iowa
          McCray Lab
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/lab_host="E.coli DHI0 B"
/note="Vector: pSPORT I; Site_1:
Directional"
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Eutheria;
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Primates;
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Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics (www.resgen.com).
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Fax: 319 356 7171
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/note="Organ: Lung; Vector: pT7T3-Pac (pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-ECI is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the corthaging of first-strand cDNA
contains a library tag
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TAG_SEQ=AAGTGCTTAC"
83 c 92 g
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TAG_TISSUE=Normal Lung
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/clone_lib="UI-CF-EC1"
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/db_xref="taxon:9606"
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                 CTTAGCTGTTAGACTGATCTGTTTGTAGCAGTTGTTTGTCTCATTTTTGCTCTCTGTGCATT 4029
                                                                                                                                                          CGGCCTCATTCTGTGAGGGAGGGGAAAGATTAGCCAAAGAGTTAATTTTCATTCCAAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGAAATTGCTTAGTCATTGTACCTTTGTCAGCAATTTTGACAGTCATTAATGTTTGTC 4472
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                                                                                      CTTAGCTGTTAGACTGATCTGTTTGTAGCAGTTGTTTGTCTCATTTTTGCTCTGTGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No rl sequence available.
This clone (DKFZp434F0915) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd. Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL040840 RRNA DKFZp434F0915_s1 434 (synonym: htes3) Homo DKFZp434F0915 3', mRNA sequence.
AL040840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German Genome Project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                  221
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ished (1999).
                                                                                                                                                                                                                                                                                                                               /Clone="DKFZp434F0915"
/Clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DHIOB"
/note="Vector: pSport1; Site_1: N
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 8.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTACTTGATATCTTGTTCTTTAAATTTTCTTCACATATGGTTTGCCTGATACAACTGAT 4149
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                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9747 row: 1 column: 14 High quality sequence stop: 557.
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 900)
                 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
                                   /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector; pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 2 kb. Library constructed by Lif
Technologies."
               Technologies
                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3918877"
/clone_lib="NIH_MGC_72"
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 695)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the 
Tissue Procurement: CLONETECH Laboratories, Inc. cDNA Library Preparation: CLONETECH Laboratories, 1 cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                          mRNA sequence.
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602251048F1 NIH_MGC_81
                                                            Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
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Query Match
Best Local Similarity 94.5
TCACATATGGTTTGCCTGATACAACTGATTTTTATAACTGAAATTTAAGGAATCTAACAG
                                                                                             GGTGCTCTACTGTATTTTTCTTTTTAATATCTACTTGATATCTTGTTCTTTAAATTTTTCT
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1214 row: o column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 3' adaptor sequence:
5'-ATTCTMGAGGCCGAGGGGCGGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palc Alto, CA)."
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/note="Organ: muscle (skeletal); Vector: pDNR-LIB
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/clone_lib="NIH_MGC_81"
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656 CTAAAACTCAGTAGGGGC 673
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                          AAGTGCATMTATTTCCTTATAACATAGACCCGTTGCTACTCTCAGCACCCTCTCCTCAAT 4252
                                                                                        TGCCTGATACAACTGATTTTTATAACTGAAATTTAAGGAATCTAACAGCTAAAACTCAGT 4192
                                                                                                                                                                             TATTTTTCTTTTAATATCTACTTGATATCTTGTTCTTTAAATTTTCTTCACACATATGGTT 4132
                                                                                                                                                                                                                                                               TTTTTGCTCTGTGCATTTTTTGAGACATTTGTTGAGAATATTCTATTTGGTGCTCTACTG
                                                                                                                                                                                                                                                                                                                                                   ATTTTCATTCCAAATCACTTAGCTGTTAGACTGATCTGTTTGTAGCAGTTGTTTTGTCTCA 497
                                                                      TGCCTGATACAACTGATTTTTATAACTGAAATTTAAGGAATCTAACAGCTAAAACTCAGT
                                                                                                                                                       TATTTTTCTTTTAATATCNACTTGATATCTTGTTCTTTAAATTTTCTTCACATATGGTT
                                                                                                                                                                                                                                           TTTTTGCTCTGTGCATTTTTTGAGACATTTGTTGAGAATATTCTATTTGGTGCTCTACTG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAATTATGGCTTGCCTGATA-AACTGGATTCTATAACTGGAATCTCAGGAAT-TAACAG
                                                                                                                                                                                                                                                                                                                                                                                                              552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hi90c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:9979552 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW665394.1 GI:7457940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //note-more pooled; Vector: pT7T3D-Pac (Pharmacia) with /note-more pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was FCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2979552"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_"0st="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%;
99.6%;
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Pred. No. 1.1e-94;
1; Mismatches 1;
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밁 Qy В δÃ 밁 δÃ Вb QΥ В ρy Db 4373 4493 TGGGTTTCAGAATA 4506 4253 4313 136 256 16 AATTATTAGAAAATGCTAATTAAGTACCAGCACATAGAAACATGAAATTGCTTAGTCATT 4432 TTTTTTTCCTGTAGCATGTGATGCCTGATTAAACTCATTTTCATTTAGCTTTTATTTCTAA TGGGTTTCAGAATA TTTTTTTCCTGTAGCATGTGATGCCTGATTAAACTCATTTTCATTTGCTTTTATTTCTAA 4312 4492 197 257

Search completed: March 22, 2003, 10:47:45 Job time: 6639 secs

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Total number of hits satisfying chosen parameters:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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       A_Geneseq_101002:*

1: /SIDS1/gcgdata/ge
2: /SIDS1/gcgdata/ge
3: /SIDS1/gcgdata/ge
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4142
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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172.5	172.5	172.5	175.5	177	180	185	185	1839	. 4142	Score
4.2	4.2	4.2	4.2	4.3	4.3	4.5	4.5	44.4	100.0	Query Match
	515							357	807	Query Match Length DB
22	16	16	16	22	15	16	15	22	23	DB
AAB49946	AAR69504	AAR69506	AAR82801	ABB62855	AAR63807	AAR73963	AAR49829	AAB94073	ABG61812	ID
A. oryzae protein	Aspergillus sp. re	Aspergillus sp. re	Bovine phospholipa	Drosophila melanog	Protein disulphide	Humicola insolens	Highly heat-resist	Human protein sequ	Prostate cancer-as	Description

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	A AC 6 A 6 A 7	AAR51696	AAR25297	AAP80664	AAG66111	AAR25296	AAG66113	AAG66107	AAG41950	AAP80615	ABB91088	ABG61000	AAW70270	ABG61002	ABG60996	AAW69726	AAU30243	AAG66531	ABB58589	AAY70762	AAY70769	AAU30491	ABB07836	AAY70770	AAG41949	AAR26174	AAY70766	AAB49944	AAB49936	AAR69505	AAR70329	ABP41717	AAB43424	AAB82539	AAE12991
Suring acta seducate	2010	n PDI.	PDI. Homo sapiens	Polypeptide with p	trans	Recombinant PDI (A	D. immitis transgl	transg	Arabidopsis thalia	Bovine protein dis	Herbicidally activ	Dirofilaria immiti	Dirofilaria immiti	Dirofilaria immiti	Dirofilaria immiti	Saccharomyces cere	Novel human secret	Human interferon-a	Drosophila melanog	Spider protein dis	Scorpion protein d	Novel human secret	Human protein iden	Scorpion protein d	Arabidopsis thalia		Spider protein dis	Protein disulfide		Aspergillus sp. re	Human phospholipas	Human ovarian anti		protein	Human protein disu

ALIGNMENTS

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	(EOSB-) EOS BIOTECHNOLOGY INC.		04-MAY-2001; 2001US-288589P.	30-APR-2001; 2001US-0847046.	24-APR-2001; 2001US-286214P.	06-APR-2001; 2001US-281922P.	16-MAR-2001; 2001US-276888P.	16-MAR-2001; 2001US-276791P.	24-JAN-2001; 2001US-263957P.	08-DEC-2000; 2000US-0733742.	08-DEC-2000; 2000US-0733288.	13-OCT-2000; 2000US-0687576.		12-OCT-2001; 2001WO-US32045.		18-APR-2002.		WO200230268-A2.		Mammalia.		Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.		Prostate cancer-associated protein #13.		15-AUG-2002 (first entry)		ABG61812;		ABG61812 standard; Protein; 807 AA.	.812	

Wilson

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Query Match
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Matches 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs organisms such as humans or other mammals (e.g. mice, sheep and dogs of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABG61800-ABG61944 represent prostate cancer-associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are
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                                                                                                                           TSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRIS
                                                                                                                                                                                                                  TVFRDRKRKLPLELTVELTEETFNATVMASDSIVLFYAGWQAVSMAFLQSYIDVAVKLKG
                                                                                                                                                                                                                                                                                                   ANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDMEGPDIDVQDDEVAE
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IYSEEDVLLLSTKYAASLPALLLARHTEGKIESIPLASTHAQDIVQIITDALLEMFPEIT
                                                                                                                                                                                                                                                                                                                                                                                                              PQQVSTVHLQLGLPLVFIVSQQATYEADRRTAEWVAWRLLGKAGVLLLLRDSLEVNIPQD
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0; Mismatches
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                        to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs define and/or diagnosis of the full-length cDNAs -
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakama
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A, Nagai K,
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                                                                                Novel protein di:sulphide isomerase active the production of 3-D active proteins
                                                                                                                                                     WPI;
                                            Claim
                                                                                                                                                                                             (TOYA ) TOYAMA
                                                                                                                                                                                                                                   27-MAY-1992;
                                                                                                                                                                                                                                                                             04-MAR-1993;
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  PDI has
                                        Page 7-8; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme;
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the following characteristics:
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  ability
                                                                                                           use
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RESULT 4
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Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalysing disulphide exchange reaction in a protein; (B) least ribonuclease A as the substrate; (C) has an optimum temp. of 20 to 70 degrees C; (D) is stable at pH 6 to 9; emol.wt. of ca. 60000 to 62000 measured by SDS-PAGE. PDI advantageously in a refolding reaction of a protein.
                                                                                                                                                            promoter;
                                                                                                                                                                        Humicola
                                                                                                                                                                                                    Humicola
                                                                                                                                                                                                                               12-JAN-1996
                                                                                                                                                                                                                                                         AAR73963;
                                                                                                                                                                                                                                                                                  AAR73963
                           JP07107980-A
                                                                 Peptide
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                                                                                                                                    Humicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 21.9
mes 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  FLQSYIDVA---VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSLEV----NIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLAEFFAPWCGHCKALAP------EYEEAATTLKEKNIKLAKVDCT-----
                                                                                                                                                                                                                                                                                                                                                     SGSRTVEDLIKFIAENG-KYKAAIS--EDAEE
                                                                                                                                                                                                                                                                                                                                                                             AGMLGTKDLLKFIQLNRISYPVNITSIQEAEE 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVLFYAGWQAVSMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFPAFAIQEVAKNQKFPFDQEKE-ITFEAIKAFVDDFVAGKIEPSIKSEPIPEKQ----
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                                                                                                                                                                          insolens;
                                                                                                                                                                                                 insolens protein disulphide isomerase.
                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                    insolens
                                                                                                                                                         insolens; protein disulphide isomerase;
recombinant production; fungal protein
                                                                                                                                                                                                                             (first entry)
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21..505
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                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                  Protein;
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                                                    mat_peptide
                                                                               sig_peptide
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Pred. No. 1.9e
79; Mismatches
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                                                                                                                                                                                                                                                                                  AA
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No. 1.9e-07;
smatches 213;
                                                                                                                                                                                                                                                                                                                                                     456
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                                                                                                                                                                          Bacillus
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RESULT 5
AAR63807
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Best Local S
Matches 112
 29-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ87670 encodes AAR73963 Humicola insolens protein disulphide isomerase (PDI). By linking a Bacillus brevis promoter to the cDNA the fungal PDI can be expressed in B. brevis cells. The recombinant PDI can then be isolated from the culture medium, with a yelld as high as 500mg/l of culture supernatant.
                                    AAR63807;
                                                                  AAR63807 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungal protein di:sulphide isomerase encoded contg. Bacillus brevis promoter - useful for large quantities of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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DB; AAQ87670.
                                                                                                                                                                              AGMLGTKDLLKFIQLNRISYPVNITSIQEAEE
                                                                                                                                                                                                                          LAPKYEELGALYAKSEFKDRVVIAKVD-ATANDV--PDEIQGFPTIKLYPAGAKGQPVTY
                                                                                                                                                                                                                                                                                           EGPVTVVVAKNYNEIVLDDTK-----
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                                                                                                                                                         SGSRTVEDLIKFIAENG-KYKAAIS--EDAEE
                                                                                                                                                                                                                                                         FLQSYIDVA---VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSY
                                                                                                                                                                                                                                                                                                                                                                                               DSLEV----NIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pages 8-11; 13pp; Japanese.
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 (first entry)
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                                                                  Protein;
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                                                                    505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ73410 encodes AAR63807 Humicola insolens protein disulphide isomerase (PDI), which was used in the construction of a vector. The vector was used to transform suitable host cells enabling them to produce PDI. PDI produced in this way had increased stability and tolerance to sulphhydryl group containing reducers, compared to PDI obtained from mammals and yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein di:sulphide isomerase (PDI) gene - encodes a PDI showing increased stability, and tolerance against a sulphydryl gp-contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 12; 15pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein disulphide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                40 LVLAEFFAPWCGHCKALAP------EYEEAATTLKEKNIKLAKVDCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1994-328999/41.
DB; AAQ74310.
                                                                                                                                                                                                      TVHLQLGLPLVFIVSQQATYEAD-----RRTAE-----WVAWRLLG-KAGVLLLLR
                                                                                                                                                                                                                                                                                                                                          LEDLQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGTTYQFVLTTEIALLESIGS 185
 FLQSYIDVA---VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSY
                                   EGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVLFYAGWQAVSMA
                                                                                                    DKFPAFAIQEVAKNQKFPFDQEKE-ITFEAIKAFVDDFVAGKIEPSIKSEPIPEKQ----
                                                                                                                                     DSLEV----NIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDM 346
                                                                                                                                                                        D-YMSAGIPLAYIFAETAEERKELSDKLKPIAEAQPGVINFGTIDAKAFGAHAGNLNLKT
                                                                                                                                                                                                                                                                       EDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAEDPQQVS
                                                                                                                                                                                                                                                                                                           LEEFKKADKA-----VLVAYVDASDKASSEVFTQVAEKLRDNYPFGSSSDAALAEAEGV 191
                                                                                                                                                                                                                                                                                                                                                                              --EETDLCQQHGVEGYPTLKVFRGLDNVSPYKGQRKAAAITSYMIKQSLPAVSEVTK-DN
                                                                                                                                                                                                                                                                                                                                                                                                             CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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1..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= sig_peptide
                                                                                                                                                                                                                                          -AIVLYKDFDEGKAVFSEKFEVEAIEKFAKTGATPLIGEIG--PETYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing reducer
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21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 180; DB 15;
Pred. No. 5.7e-07;
0; Mismatches 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 505;
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PM 27-S
XX W Phar
XX Vent
XX Vent
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                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEV 2000 co. Isolated nucleic acid detection reagent.

The invention relates to an isolated nucleic acid detection reagent invention of Antanting 1000 or more genes from Drosophila. The invention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB62855 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462
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                  484
                                                                                       424
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                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSRTVEDLIKFIAENG-KYKAAIS--EDAEE 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAPKYEELGALYAKSEFKDRVVIAKVD-ATANDV--PDEIQGFPTIKLYPAGAKGQPVTV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-656860/75.
DB; ABL06958.
                  NITSIQEAEEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYS
                                                                                                                                                           ELTVELTEETFNATV-----MASDSIVL--FYAGWQAVSMAFLQSYIDVAVKL-KGTST 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGMLGTKDLLKFIQLNRISYPVNITSIQEAEE
                                                    IKLAKVDATVEGELAEQYAVRGYPTLKFFRSG-SPVEYSGGRQAADIIAWVTKKTGPPAK 138
                                                                                     MLLTRINCADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPV
                                                                                                                           EAEVKVEEGVLVATVDNFKQLIADNEFVLVEFYAPWCGHCKALAPEYAKAAQQLAEKESP
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                                                                                                                                                                                                  99;
                                                                                                                                                                                                Similarity 19.1
99; Conservative
                                                                                                                                                                                                                                                                       496
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                  96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496
                                                                                                                                                                                                                 Score 177; DB 2
Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers
                                                                                                                                                                                                Mismatches 180;
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AAR82801
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                QΥ
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Best Local S
Matches 66
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                                                                                                                           Sequence
                                                                                                                                                              measure
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT00952.
                                                                                                                                                                                                                                                                                                                                          WPI; 1995-139593/18
                                                                                                                                                                                                                                                                                                                                                                            Hirai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phospholipase
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                                                                                                                                                                                                                                   Example 1; Page 25-29; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9508624-A
                                                                                                                                                                                                                                                                       inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                             (SHIO ) SHIONOGI & CO LTD
446
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                                                                                                                                                              cancer
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                            Hirano N;
                                              4.2%;
milarity 23.3%;
Conservative 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c;
                                                                                                                           A.
                                                                                                                                                            progression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLC; alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      801
                                                      56;
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AAR82801 is bovine phospholipase C-alpha (PLC-alpha). PLC-alpha can be used as an anti-inflammatory and may also be used to
                                                                                                                                                                                                                                                                                           Human phospholipase C-alpha and DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIEKYVDPLKEIAKKYRDDILFVTISSDEEDHTRIFEFFGMNKEEVPTIRLIKLEEDMAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLTSVADAEQFL-----KD----NEIAIIGFFKDLESEEAKTFTKVANALDSFVF-GVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVLVEFYAPWCGHCKQLAPIYDQLAEKYKDNEDIVIAKMDSTANELESIKISSFPTIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSQRGTRKVP---KCMKETDVQENDKEQHEDKSAV-----RKEPIETLRIKHWNRSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKKFAQVQSLPLIVDFNHESASKIFGGSIKSHLLFFVSRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPSYFRLQK-PLLILFSDGTVNPQY----KKAILTLVKQKYLDSFTPCWLNLKNTPVGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILRAYFDPLPPLPL-----LVLVNLHSGGQ----VFAF-----
Score 175.5; DB 16
Pred. No. 1.4e-06;
6; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory; cancer.
                                               DB 16;
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  Indels
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                                            Length
                                                                                                                                                                                                                                                                                                  as anti
                                               505;
    33;
  Gaps
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431

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RESULT 8
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                                                          Query Match 4.2%; Score 172.5; DB 16; Best Local Similarity 19.9%; Pred. No. 2.7e-06; Matches 105; Conservative 107; Mismatches 185;
                                                                                                                                                      This sequence encodes a protein-disulfide-isomerase (PDI) which is useful for treatment or degradation of scleroproteins, which is useful for treatment or degradation of scleroproteins, especially hair, skin and wool, etc. The protein is prepared recombinantly from Aspergillus oryzae IFO 4177 or Aspergillus niger A524. The protein may be truncated into various peptides, all with PDI activity. This protein differs from AAR69505 in that AA 511 is Ala not Glu.
                                                                                                                                                                                                                                                                                                              Protein di-sulphide isomerase enzyme - obtd. from Aspergillus, useful for e.g. treating scleroproteins such as human hair or for fabric cleaning
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-052073/07.
N-PSDB; AAQ81934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR69506;
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                  Disclosure; Page 10; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             Hjort CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein-disulfide-isomerase; enzyme; scleroprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR69506 standard; Protein; 511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9500636-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                filamentous fungus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus sp. recombinant protein-disulfide-isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552 TKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVENLP 605
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                             15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEE-ISR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
LVLAEFFAPWCGHCKALAP-KY------EQAATELKEKNIPLVKVDCTEEEALCR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LLQGKDLLIAYYDVDYEKNAKGSNYWRNRVMMVAKKFLDA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKFISDK-----DASVVGFFKDLFSEAHSEFLKAASNLRD---NYRFAHTNVESLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLS 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANTNTCNKYGVSGYPTLKIFRDGEESGAYDGPRTADGIVSHLKKQAGPASVPLKSEEEF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LELTDDNFESRITDTGSSGLMLVEFFAPWCGHCKKLAPEYEAAATRLKG--IVPLAKVDC
                                                                                                                          511 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93DK-0000768
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                                                            Indels 131;
                                                                                        Length 511;
                                                          Gaps
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Qy	74 YCGKEKDLMKAYLFKGNILLREPPTDTLFDVNAIVAHVLFALLFSEVKYITNLE 127	7
DЬ	FRGLDAVKPYQGARQTEAIVSYMVKQSL-PAVSPVTPE	7
Qy	LQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGTTYQFVLTT	0
Дb	TTFAESQRDNYLFAATSDAS	4
Qy	EYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTE	0
Db	195 KAEGVKQPSIVLYKDFDEKKATYDGEIEQDALLSWVKTASTPLVGEIG 242	2
Qy	LQLGLPLVFIVSQQATYEADRRTA	8
Db	LA .	0
Qγ	013	4
Db	291DAKLYGAHA-GNLNLDPSKFPAFAIQDPEKNAKYPYDQ 327	7
Qy	VFRDRKRKLPLELTVELTEETFNATVMASDSIV 39	4
Db	IGKFIQDVLDDKVEPSIKSEAIPETQEGPVTVVVAHSYKDLVLDNEKDV 38	4
Qy	AGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMY 45	N
DЪ	385 LLEFYAPWCGHCKALAPKYEELASLYKDIPEVTIAKĮD-ATANDVPDSITGFPTIKLF 441	\vdash
Qy	LGTKDLLKFIQLNRISYPVNITSIQEAEEYLS	
Db	442 AAGAKDSPVEYEGSRTVEDLANFVKENG-KHKVDALEVDPKKEQESGD 488	
8 S	JLT 9 9504 AAR69504 standard; Protein; 515 AA.	
X 25 X	AAR69504;	
¥ 53 \$	18-AUG-1995 (first entry)	
Z E S	Aspergillus sp. recombinant protein-disulfide-isomerase.	
X X X	Protein-disulfide-isomerase; enzyme; scleroprotein; filamentous fungus.	
S S	Aspergillus.	
Y P N	WO9500636-A.	
X PD	05-JAN-1995.	
X P	28-JUN-1994; 94WO-DK00266.	
y PR	28-JUN-1993; 93DK-0000768.	
X P R	(NOVO) NOVO-NORDISK AS.	
X P	Hjort CM;	
Y DR	WPI; 1995-052073/07. N-PSDB; AAQ81933.	
TG	Protein di-sulphide isomerase enzyme - obtd. from Aspergillus, useful for e.g. treating scleroproteins such as human hair or for fabric cleaning	
X P S	Disclosure; Page 32; 61pp; English.	
88	encodes a protein-disulfide-isomerase (PI	
88	ially hair, skin and wool, etc. The protein is prepared binantly from Aspergillus oryzae IFO 4177 or Aspergillus	

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              niger A524. The protein may all with PDI activity.
            (NOVO ) NOVO
                                   18-MAY-1999;
02-JUN-1999;
                                                          17-MAY-1999;
                                                                                                           23-NOV-2000
                                                                                                                                  WO200070064-A1
                                                                                                                                                       Aspergillus
                                                                                                                                                                                Disulphide bond; allergy; food additive; cosmetic.
                                                                                                                                                                                                                     A. oryzae protein disulfide isomerase
                                                                                                                                                                                                                                             07-MAR-2001
                                                                                                                                                                                                                                                                    AAB49946;
                                                                                                                                                                                                                                                                                           AAB49946
                                                                                  17-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEE-ISR 73 ::: |: | :| |:| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGT-----TYQFVLTTEIALL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQGVE-----GYPTLKIFRGLDAVK--PYQGARQTEAIVSYMVKQSL-PAVSPVTPENLE
                                                                                                                                                                                                                                                                                                                                                                                                  LLEFYAPWCGHCKALAPKYEELASLYKDIPEVTIAKID-ATANDV-~PDSITGFPTIKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKEVKAKDIGKFIQDVLDDKVEPSIKSEAIPETQEGPVTVVV---AHSYKDLVLDNEKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DMEGPDI-----DVQDDEVAETVFRD---RKRKLPLELTVELTEETFNATVMASDSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAEGVKQP-----SIVLYKDFDEKKATYDGEIEQDALLSWVKTASTPLVGELG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESIGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIKTMDKI-----VVIGYIASDD-----QTANDIFTTFAESQRDNYLFAATSDASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVLAEFFAPWCGHCKALAP-KY------EQAATELKEKNIPLVKVDCTEEEALCR
                                                                                                                                                                                                                                                                                                                                                    AAGAKDSPVEYEGSRTVEDLANFVKENG-KHKVDALEVDPKKEQESGD
                                                                                                                                                                                                                                                                                                                                                                          KKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGE 498
                                                                                                                                                                                                                                                                                                                                                                                                                           L--FYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMY 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIE-----EIQEDEDN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PETYSG-YITAGIPLAYIFA-ETKEEREQFTEEFKFIAEKHKGSINIVTI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQQVSTVHLQLGLPLVFIVSQQATYEADRRTAE---WVAWRLLGKAGVLLLLRDSLEVNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCGKEKDLMKAY - - - - LFKGNILLREFPTDTLFDVNAIVAHVLFALLFSEVKYIT - - NLE
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105; Conserv
                                                                                                                                                                                                                                                                                           standard;
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            NORDISK AS
                                                                                  2000WO-DK00265
                                                                                                                                                                                                                                             (first entry)
                                   99DK-0000683.
99DK-0000689.
99US-0137068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DAKLYGAHA-GNLNLDPSKFPAFAIQDPEKNAKYPYDQ
                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%;
19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107;
                                                                                                                                                                                             protein disulfide
                                                                                                                                                                                                                                                                                           515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 172.5; DB 16;
Pred. No. 2.7e-06;
)7; Mismatches 185;
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                                                                                                                                                                                             isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                     488
                                                                                                                                                                                             variant;
                                                                                                                                                                                            detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 11 AAE12991

standard;

Protein;

515

X X X D X D X A X

AAE12991 sta AAE12991; 28-JAN-2002

(first

entry)

Human protein disulphide isomerase (PDI).

Heat shock protein; HSP; HSP peptide-binding fragment; HPBF; vaccine; cytotoxic T cell response; hepatitis virus; herpes simplex virus;

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Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides variants of the Aspergillus oryzae prodisulfide isomerase enzyme. These are capable of reducing disulphide bonds in proteins, which may be the cause of allergies in humans. The proteins can be used to reduce the allergenicity of foods, to treat scleroproteins, in detergents, in food additives and in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein disulfide isomerase variant having increased reducing properties and decreased redox potential than native proteins, used to reduce allergenicity of allergic proteins in feed, food or cosmetic products -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 72-74; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC89028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hjort CM;
442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEE-ISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 LVLAEFFAPWCGHCKALAP-KY------EQAATELKEKNIPLVKVDCTEEEALCR 95
                  KKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGE
                                                                                                                                                                                                                                                                               PQQVSTVHLQLGLPLVFIVSQQATYEADRRTAE--WVAWRLLGKAGVLLLLRDSLEVNIP
                                                                                                                                                                                                                                                                                                                                                    ESIGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAED
                                                                                                                                                                                                                                                                                                                                                                                                                DLQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGT-----TYQFVLTTEIALL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                DQGVE-----GYPTLKIFRGLDAVK--PYQGARQTEAIVSYMVKQSL-PAVSPVTPENLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCGKEKDLMKAY - - - - LFKGNILLREFPTDTLFDVNAIVAHVLFALLFSEVKYIT - - NLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-070776/08
AAGAKDSPVEYEGSRTVEDLANFVKENG-KHKVDALEVDPKKEQESGD
                                                             LLEFYAPWCGHCKALAPKYEELASLYKDIPEVTIAKID-ATANDV--PDSITGFPTIKLF
                                                                                           L--FYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMY
                                                                                                                           SKEVKAKDIGKFIQDVLDDKVEPSIKSEAIPETQEGPVTVVV----AHSYKDLVLDNEKDV
                                                                                                                                                                                                                        QDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIE-----EIQEDEDN------
                                                                                                                                                                                                                                                      PETYSG-YITAGIPLAYIFA-ETKEEREQFTEEFKFIAEKHKGSINIVTI------
                                                                                                                                                                                                                                                                                                                      KAEGVKQP-----SIVLYKDFDEKKATYDGEIEQDALLSWVKTASTPLVGELG--
                                                                                                                                                                                                                                                                                                                                                                                   EIKTMDKI-----VVIGYIASDD------QTANDIFTTFAESQRDNYLFAATSDASIA
                                                                                                                                                       --DMEGPDI-----DVQDDEVAETVFRD----RKRKLPLELTVELTEETFNATVMASDSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 19.9
05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DAKLYGAHA-GNLNLDPSKFPAFAIQDPEKNAKYPYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                               498
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                                                                                               452
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                                                                                                                                                                                                                                        CC peptide binding fragments of heat shock proteins (HSPS) and non-
CC covalent complexes of HSP peptide-binding fragments (HSPS) and non-
CC covalent association with antigenic may be used to stimulate an
CC peptide fragments of the invention may be used to stimulate an
CC influenca varicella, adenovirus, herpes simplex (HSV) type I and
CC type II, rinderpest rhinovirus, echovirus, rotavirus, respiratory
CC syncytial virus, mumps virus, papova virus, papilloma virus,
CC arbovirus, cytomegalovirus, echovirus, huntavirus, coxsackie virus,
CC measles virus, rubella virus, pollo virus, HIV-I, and HIV-II;
CC measles virus, rubella virus, pollo virus, HiV-I, and HIV-II;
CC measles virus, rubella virus, pollo virus, huntavirus, woxplasma,
CC meisseria and Legionella); protozoa (including Leishmani, Kokzidioa
CC and Trypanosoma) and intracellular parasites (including Chlamydia and
CC Rickettsia). The vaccines may be used to treat cancers such as human
CC sarcomas and carcinomas, pancreatic cancer, breast cancer, ovarian
CC adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma,
CC papillary carcinoma, papillary adenocarcinomas, medullary carcinoma,
CC Cystadenocarcinoma, bronchonenic carcinoma, renal carli carcinoma,
CC Cystadenocarcinoma, bronchonenic carcinoma, renal carli carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human immu
protozoa;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                        hepatoma, bile duct carcinoma, choriocarcinoma, seminoma and embryonal carcinoma. The present sequence is human protein disulphide isomerase (PDI), a HSP involved in folding of many disulphide-bonded proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine compositions for vaccinating against cancers and infections, comprises peptide-binding fragments (PBFs) of heat shock proteins (HSPs) and non-covalent complexes of PBFs of HSPs and antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2001
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                                                                                                                                                                                                                                                                                                                                cystadenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to pharmaceutical compositions comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-2000; 2000US-0488393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sarcoma; carcinoma;
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                    88
                                                      75
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                                                                                                                                                                                  Local Similarity
                                                                                                                           VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY 74
                                                        CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN
                                                                                         LVLAEFFAPWCGHCKALAP-KY------EEAATELKAKNIPLVKVDCTAEE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency virus; bacteria; Mycobacteria; Rickettsia;
zoa; Leishmani; Trypanosoma; intracellular parasite; Chlamydia;
ma; carcinoma; cancer; human; protein disulphide isomerase; PDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRIVASTAVA P K.
                      DLCRSQGVEGYPTLKIFRGVDSSKPYQGARQTESIVSYMIKQSLPAVSSVNE-EN
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213..3
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1..370
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                                                                                                                                                                                                                                                                                                                            bronchogenic carcinoma, renal cell carcinoma,
                                                                                                                                                                                4.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                               89;
                                                                                                                                                               Score 169.5; DB 22; Pred. No. 5.1e-06; 9; Mismatches 193;
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                                                                                                                                                                                                  Length
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                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82539
                                                                                              (UYCO-) UNIV CONNECTICUT HEALTH
                                                                                                                     20-JAN-2000; 2000US-0488393
                                                                                                                                          18-JAN-2001; 2001WO-US01781
                                                                                                                                                                                    WO200152791-A2
                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                       immunotherapy;
                                                                                                                                                                                                                                                                                                                                                  Protein disulfide isomerase; PDI; human; heat shock protein; HSP;
                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82539 standard;
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                                                     2001-457506/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGFPTLRLYPAGAKDSPIEYSGSRTVEDLANFVKENG-KHNVDALNVASEETQEGGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEFPIIKMYKKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APWCGHCKALAPKYDELAALY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTK-------QNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDEDNDMEGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVL--FY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETYSG-YIGAGVPLAYIFA-ETKEEREKYTEDFKPIAQKHKGAINIATIDAKMFGAHAGN
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                                                                                                                                                                                                                                                                                                                                                                         disulfide isomerase
                                                                                                                                                                                                                                                                                                                                        therapy; cancer;
                                                                                                                                                                                                                    /note= "
204..491
                                                                                                                                                                                                                                          /note= "
213..351
                                                                                                                                                                                                                                                              /note= "peptide-binding 5..232
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                                                                                                                                                                    "peptide-binding
                                                                                                                                                                                                         "peptide-binding
                                                                                                                                                                                                                              "peptide-binding
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                                                                                                CENT
                                                                                                                                                                                                                                                                                                                                         infection; vaccine
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Pharmaceutical composition, used to treat or prevent infection cancer, comprises a complex comprising a heat shock protein-bit fragment associated with a molecule displaying antigenicity of infectious agent or cancer cell.

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AAB43424
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating or preventing cancer/infectious disease involve culturing a cancer cell/infected cell transformed with a nucleic acid encoding a HSP peptide-binding domain, recovering complexes of the HSP fragments noncovalently associated with peptides from the cancer cell/infected cell, and administering the recovered complexes. These methods can use PDI peptide-binding fragments comprising amino acids 5-232, 213-351 and 204-491 of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid) peptides, and a larger fragment, including amino acids 204-491, which is able to bind polypeptides of 25-50 amino acids. An even larger fragment, including amino acids 1-370 is required for more complex substrates, such as larger polypeptides. The invention relates to complexes of peptide-binding fragments of HSPs with antigenic molecules and their use in immunotherapy for the treatment of infectious diseases and cancer. Claimed methods of
                  AAB43424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                  AAB43424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contribute to peptide binding, including a fragment that includes amino acids 213-351 and is capable of binding short (10-15 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PDI), a heat shock protein (HSP) involved in the folding disulfide-bonded proteins. PDI contains various domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 53;
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                                                                                                                                      TGFPTLRLYPAGAKDSPIEYSGSRTVEDLANFVKENG-KHNVDALNVASEETQEGGDV
                                                                                                                                                                     TEFPIIKMYKKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGEL 499
                                                                                                                                                                                                                                           AGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTK-------QNV 443
                                                                                                                                                                                                                                                                                                                EDEDNDMEGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVL--FY 397
                                                                                                                                                                                                                                                                                                                                                   LNLDSQKFPAFAIQDPAKNAKYPYDQAKELNADEVEKFI----QDVLDGKVEPSIKSEPVP
                                                                                                                                                                                                                                                                                                                                                                                   LLLLRDSLEVNIPQD----ANVVFKRAEE--GVPVEFLVLHDVDLIISHVENNMHIEEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQVSTVHLQLGLPLVFIVSQQATYEADRRTAEW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQPSIV-LYKDFDEKKAVYDGEIEQEA------IHSWVKSASTPLVGEIG--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----DLCRSQGVEGYPTLKIFRGVDSSKPYQGARQTESIVSYMIKQSLPAVSSVNE-EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN
                                                                                                                                                                                                            APWCGHCKALAPKYDELAALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDVEYAHLY - - FFHCKLVLD - - LTQQCRRTLMEQPLTTLNIHLF IKTMKAPLLTEVAEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEEIKTMDKI-----VVIGYIPSDDQETYQAFEKYAESQRDNYLFAATDDAAIAKSEGV
                                                                                                                                                                                                                                                                              Similarity
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                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 68
                                                  544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 169.5; I
Pred. No. 5.1e
89; Mismatches
                                                  B
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                                                                                                                                                                                                         ADHPDLAAKVTIAKIDATANDVPDPI 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VAWRLLG-KAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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67

125

432 ADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEA 491

TANTINTCNKYGVSGYPTLKIFRDGEEAGAYDGPRTADGIVS--HLKKQAGPASVPLRTEE

376 VELTEETFNATVMASDS----IVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINC

LELTDDNFESRISDTGSAGLMLVEFFAPWCGHCKRLAPEYEAAATRLKG--IVPLAKVDC

124

Best Matches Query Match

Local

l Similarity 64; Conser

Conservative

59;

4.1%; 22.6%;

Score 169.5; Pred. No. 5.0 Mismatches

.6e-06; les 127;

Indels Length

Gaps

10;

DB 21;

544; 33;

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agonists
AAC78457
                                                                                                                                       or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate
                                                                                                                                                                                                                      polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                  AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammatio immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                    antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; cytostatic; antidiabetic; antiasth
Sequence
                                                                            inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC77633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing {\tt e.g.} cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer associated protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN
                                      present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                       and AAB44240 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 1424-1426; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM
  544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US05882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tostatic; proliferative; vulnerary; immunomodulator;
antiasthmatic; antirheumatic; antiarthritic; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated gene; cancer antigen; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO:869
                                                         exemplification
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                                                         AAC78449 to fication of
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RESULT 14
ABP41717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                               treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, an metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chamydia, HIV, toxoplasmosis, and toxic the content of the con
                                                                                                                                                                                                                                                                                                                            The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABC94131-ABC56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen
                                                               shock
                                                                                                                                                                                                                                                                     polynucleotides, antibodies against human ovarian antigens, and to of ovarian antigen polynucleotides and polypeptides in diagnosing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; urinary system disorder; drug screening; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                              vaginitis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system diso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABQ54794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-147878/19.
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                                                            syndrome),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian antigen HPDRV42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune disorders,
eases -
                                                      inflammatory conditions (e.g., mastitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gynaecological;
                                    disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549
                           (e.g.,
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                                 congenital
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug trargeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from WIPO
Hirai H,
                                                                                                                                                                                                                                                                                                                                     Human phospholipase
                            (SHIO ) SHIONOGI & CO
                                                             24-SEP-1993;
                                                                                          22-SEP-1994;
                                                                                                                          30-MAR-1995
                                                                                                                                                      W09508624-A
                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                        Phospholipase C;
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                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LIQGKDLLIAYYDVDYEKNAKGSNYWRNRVMWVAKKFLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS
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1..24
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                                                                                                                                                                                                                                                                                                        PLC; alpha; anti-inflammatory; cancer.
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Pred. No. 5.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 21-24; 39pp; Japanese.
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N-PSDB; AAQ86642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human phospholipase C-alpha and DNA encoding it - useful as anti inflammatory % \left( 1\right) =\left\{ 1\right\} =\left\{ 1
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---LIQGKDLLIAYYDVDYEKDAKGSNYWRNRVMVAKKFLDA 293
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135.5 3.3 509 2 US-08-557-122A-27 Sequence 27, Appl 135.5 3.3 509 4 US-08-66-27 Sequence 27, Appl 135.5 3.3 468 4 US-08-874-102-33 Sequence 37, Appl 135 3.3 472 4 US-08-874-102-55 Sequence 55, Appl 135 3.3 497 4 US-08-874-102-55 Sequence 37, Appl 135 3.3 497 4 US-08-874-102-78 Sequence 38, Appl 135 3.3 510 2 US-08-557-122A-28 Sequence 28, Appl 133.5 3.2 638 4 US-09-262-666-28 Sequence 28, Appl 133.5 3.2 638 4 US-09-262-666-38 Sequence 38, Appl 133.5 3.2 638 4 US-09-262-666-38 Sequence 38, Appl 133.5 3.2 510 2 US-08-557-122A-38 Sequence 38, Appl 133.5 3.2 510 2 US-08-557-122A-38 Sequence 38, Appl 133.5 3.2 510 2 US-08-557-122A-36 Sequence 36, Appl 131.5 3.2 364 3 US-09-134-001C-4959 Sequence 36, Appl 131.5 3.2 364 3 US-09-138-318-4 Sequence 47, Appl 131.5 3.2 364 3 US-09-138-318-4 Sequence 47, Appl 131.5 3.2 364 3 US-08-23-536A-12 Sequence 57, Appl 129.5 3.1 281 4 US-09-262-666-5 Sequence 57, Appl 129.5 3.1 281 4 US-09-262-666-5	45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	ω μ	30	29	28
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ALIGNMENTS

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ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,395A
FILING DATE: 1930527
CLASSIFICATION DATA:
APPLICATION NUMBER: JP 4-135254
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-44013
FILING DATE: Q1-MAY-1992
PRIOR APPLICATION NUMBER: JP 5-44013
FILING DATE: Q1-MAR-1993

PRIOR APPLICATION NUMBER: JP 5-44013
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Patent No. 5496719
                                                                   FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 5-44014
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5496719man F.
REGISTRATION NUMBER: 24,618
                     REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 68-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KAJINO, TSUTOMU
APPLICANT: IMAEDA, TAKAO
APPLICANT: SARAI, KIYOKO
TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
TITLE OF INVENTION: PRODUCING THE SAME
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TELEPHONE:
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IDEKOBA, CHIE
HOSHINO, FUMIHIKO
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ASAMI, OSAMU
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                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08464365 Patent No. 5700659
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                        APPLICANT:
                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                             APPLICANT: SARAI, KIYOKO
TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
TITLE OF INVENTION: PRODUCING THE SAME
                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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TYPE: a
   STREET:
                     ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT. ADDRESSEE: P.C.
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 1755 S.
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KAJINO, TSUTOMU
IMAEDA, TAKAO
SARAI, KIYOKO
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HOSHINO, FUMIHIKO
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Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                       OSAMU
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5700659man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 68-22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-
FILING DATE: 04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 4-
FILING DATE: 27-MAY-1992-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
 371
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 LVLAEFFAPWCGHCKALAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
LAPKYEELGALYAKSEFKDRVVIAKVD-ATANDV--PDEIQGFPTIKLYPAGAKGQPVTY
                                       FLQSYIDVA---VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSY 461
                                                                                                                                                                                                                                D-YMSAGIPLAYIFAETAEERKELSDKLKPIAEAQRGVINFGTIDAKAFGAHAGNLNLKT
                                                                                                                                                                                                                                                                    TVHLQLGLPLVFIVSQQA-----
                                                                                                                                                                                                                                                                                                       KAP-----AIVLYKDFDEGKAVFSEKFEVEAIEKFAKTGATPLIGEIG--PETYS
                                                                                                                                                                                                                                                                                                                                                                                 LEEFKKADKA-----VLVAYVDASDKASSEVFTQVAEKLRDNYPFGSSSDAALAEAEGV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                          --EETDLCQQHGVEGYPTLKVFRGLDNVSPYKGQRKAAAITSYMIKQSLPAVSEVTK-DN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN 125
                                                                            EGPVTVVAKNYNEIVLDDTK------
                                                                                                               EGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVLFYAGWQAVSMA 406
                                                                                                                                                      DKFPAFAIQEVAKNQKFPFDQEKE-ITFEAIKAFVDDFVAGKIEPSIKSEPIPEKQ----
                                                                                                                                                                                         DSLEV----NIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDM
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7: U.S.A.
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: (703) 413-2220
248855 OPAT UR
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21.9%; Pred
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Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                    -----TYEADRRTAEW--VAWRLLG-KAGVLLLLR 290
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                                                                              -DVLIEFYAPWCGHCKA
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Gaps

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                                                   Best Local Similarity Matches 112; Conserv
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                                                                              Query Match
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                                                                                                                                                                        TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5
FILING DATE: 04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
TITLE OF INVENTION: PRODUCING THE SAME
                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                             TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                NAME: Oblon, No. 5496719man F.
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19930
40
                         15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY 74
                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 68
                                                                                                                                                                                                                                                                  NAME: Oblon, No. 54
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 4 FILING DATE: 27-MAY-1992
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LVLAEFFAPWCGHCKALAP-----
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1755 S. Jefferson Davis Highway, Suite 400
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IMAEDA, TAKAO
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04-MAR-1993
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                                                   Score 185; DB 1; I
Pred. No. 1.9e-08;
9; Mismatches 213;
-EYEEAATTLKEKNIKLAKVDCT----
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                                                   Indels 108;
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US-08-464-365-3
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                                                                 FILING DATE:
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مام 5700659
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                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4
FILING DATE: 27-MAY-1992
                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
TITLE OF INVENTION: PRODUCING THE SAME
PRIOR APPLICATION DATA:
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                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                              CLASSIFICATION: 435
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 -- EETDLCQQHGVEGYPTLKVFRGLDNVSPYKGQRKAAAITSYMIKQSLPAVSEVTK-DN
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ASAMI, OSAMU
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IMAEDA, TAKAO
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IDEKOBA, CHIE
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APPLICATION NUMBER: JP 5 FILING DATE: 04-MAR-1993 PRIOR APPLICATION DATA:

JP 5-44013

APPLICATION NUMBER:

JP 5-44014

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RESULT 5
US-08-627-907A-4
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                                                                                                      Sequence 4, Application US/08627907A Patent No. 6060302 GENERAL INFORMATION:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 68
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 413-3000
NUMBER OF SEQUENCES:
                               TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA TITLE OF INVENTION: SEQUENCE ENCODING THE SAME
                                                                APPLICANT: HIRANO, Naoto APPLICANT: HIRAI, Hisamaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5700659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  448
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                                                                                                                                                                                                                                SGSRTVEDLIKFIAENG-KYKAAIS--EDAEE 476
                                                                                                                                                                                                                                                                  AGMLGTKDLLKFIQLNRISYPVNITSIQEAEE 493
                                                                                                                                                                                                                                                                                                                                      FLQSYIDVA---VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSY
                                                                                                                                                                                                                                                                                                                                                                             EGPVTVVAKNYNEIVLDDTK - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAP-----AIVLYKDFDEGKAVFSEKFEVEAIEKFAKTGATPLIGEIG--PETYS
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ADDRESS
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21.9%; Pred. No. 1
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Mismatches
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                                                  AND DNA
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                                                                                                                             Sequence 4, Application US/08557122A Patent No. 5879664 GENERAL INFORMATION:
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Best Local S
Matches 66
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                                                 APPLICANT: Hjort, Cars
TITLE OF INVENTION: FU
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHEN-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 5-238402
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-SEP-1994 ATTORNEY/AGENT INFORMATION:
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STREET:
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                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                     ---LLQGKDLLIAYYDVDYEKNAKGSNYWRNRVMMVAKKFLDA
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                                                                                                                                                                                                                                                                                                         SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS 642
                                                                                                                                                                                                                                                                                                                                               NKYDDDGEGITLFRPSHLTNKFEDKTVAYTEQKMTSGKIKRFIQENIFGICPHMTEDNKD
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(212) 59
405 Lexington Avenue, 64th Floor
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                                     No. 58796640 No. 5879664disk of No. 5879664th America, Inc
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                                                                                                               Carsten Mailand
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                                                                                           Fungal Protein
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New York

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RESULT 7
US-09-262-666-4
; Sequence 4, Application US/09262666
; Patent No. 6346244
; GENERAL INFORMATION:
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Best Local Similarity
Matches 105; Conserv
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 39
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 YCGKEKDLMKAY----LFKGNILLREFPTDTLFDVNAIVAHVLFALLFSEVKYIT---NLE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-DEC-1995
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                                                                                                                                                                  KKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGE 498
                                                                                                                                                                                                                LLEFYAPWCGHCKALAPKYEELASLYKDIPEVTIAKID-ATANDV--PDSITGFPTIKLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQGVE-----GYPTLKIFRGLDAVK--PYQGARQTEAIVSYMVKQSL-PAVSPVTPENLE 147
                                                                                                                                        AAGAKDSPVEYEGSRTVEDLANFVKENG-KHKVDALEVDPKKEQESGD 488
                                                                                                                                                                                                                                                 L--FYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMY 452
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                                                                                                                                                                                                                                                                                                                            --DMEGPDI-----DVQDDEVAETVFRD----RKRKLPLELTVELTEETFNATVMASDSIV 394
                                                                                                                                                                                                                                                                                                                                                                                                   QDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIE-----EIQEDEDN-----
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
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CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0: FILING DATE: 11-DEC-1995 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hjort, Carsten Mailand TITLE OF INVENTION: Fungal Protein Disulfide NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                   395 L--FYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMY 452
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TOPOLOGY:
                                                                                                                                                                                   299 QDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIE-----EIQEDEDN-----
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TELEPHONE: 212-878-9655
TO TO NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEE-ISR 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
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les 105; Conserv
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LLEFYAPWCGHCKALAPKYEELASLYKDIPEVTIAKID-ATANDV--PDSITGFPTIKLF
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                                                                                                                                                                                                                                                                                                   KAEGVKQP--
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                                                                                                          --DMEGPDI-----DVQDDEVAETVFRD---RKRKLPLELTVELTEETFNATVMASDSIV
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10174-6401
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US-08-557-122A-3
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GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212.867-0123
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
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CITY: New York
                                                                                                                                                                                                                                                                                                                                          96
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TYPE: amino acid
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                               48 LVLAEFFAPWCGHCKALAP-KY-------EQAATELKEKNIPLVKVDCTEEEALCR 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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--DMEGPDI-----DVQDDEVAETVFRD---RKRKLPLELTVELTEETFNATVMASDSIV 394
                                                                                                                                                 PQQVSTVHLQLGLPLVFIVSQQATYEADRRTAE--WVAWRLLGKAGVLLLLRDSLEVNIP 298
                                                                                                                                                                                       KAEGVKQP-----SIVLYKDFDEKKATYDGEIEQDALLSWVKTASTPLVGELG--
                                                                                                                                                                                                                           ESIGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAED 240
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                                                                            QDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIE-----EIQEDEDN-----
                                                                                                                PETYSG-YITAGIPLAYIFA-ETKEEREQFTEEFKFIAEKHKGSINIVTI-------
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19.9%; Pred. No. 2.8e-07;
rative 107; Mismatches 185
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; MOLECULE TYPE:
US-08-557-122A-34
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lambiris, Elias J.
REGISTATION NUMBER: 33.728
REFERENCE, DOCKET NUMBER: 39!
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CITY: New York
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                                                                                                                                                                                                                                                                        48 LVLAEFFAPWCGHCKALAP-KY------EQAATELKEKNIPLVKVDCTEEEALCR 95
                                                                                                                                                                                                                                                                                                           15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEE-ISR 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America ZIP: 10174-6401
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                                         KAEGVKQP-----SIVLYKDFDEKKATYDGEIEQDALLSWVKTASTPLVGELG--
                                                                                                                    EIKTMDKI-----VVIGYIASDD------QTANDIFTTFAESQRDNYLFAATSDASIA 194
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PQQVSTVHLQLGLPLVFIVSQQATYEADRRTAE--WVAWRLLGKAGVLLLLRDSLEVNIP 298
                                                                            ESIGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAED 240
                                                                                                                                                   DLQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGT-----TYQFVLTTEIALL 180
                                                                                                                                                                                               DQGVE-----GYPTLKIFRGLDAVK--PYQGARQTEAIVSYMVKQSL-PAVSPVTPENLE
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19.9%;
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                                                                                                                                                                                                                                                                                                                                               Score 172.5; DB 2;
Pred. No. 2.8e-07;
7; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                      Length
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US-09-262-666-3
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Patent No. 6346244
GENERAL INFORMATION:
                                                                                                                                                   Query Match 4.2%; Score 172.5; DB 4; Length 515; Best Local Similarity 19.9%; Pred. No. 2.8e-07; Matches 105; Conservative 107; Mismatches 185; Indels 131
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INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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CORRESPONDENCE ADDRESS
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                              74 YCGKEKDLMKAY----LFKGNILLREFPTDTLFDVNAIVAHVLFALLFSEVKYIT--NLE 127
                                                                      48 LVLAEFFAPWCGHCKALAP-KY------EQAATELKEKNIPLVKVDCTEEEALCR 95
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STATE: New York
96 DQGVE-----GYPTLKIFRGLDAVK--PYQGARQTEAIVSYMVKQSL-PAVSPVTPENLE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                             VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEE-ISR 73::: |: | : | : | : | : | : | : |
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PETYSG-YITAGIPLAYIFA-ETKEEREQFTEEFKFIAEKHKGSINIVTI------
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    No. 63462440 No. 6346244disk of No. 6346244th America,
    Lexington Avenue, 64th Floor

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VENTION: Fungal Protein Disulfide Isomerase
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                                                                                                                                                     Indels 131;
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US-08-627-907A-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HIRANO, Naoto
APPLICANT: HIRAI; Hisamaru
                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                     FILING DATE: 24-SEP-PRIOR APPLICATION DATA:
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-238402
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND TITLE OF INVENTION: SEQUENCE ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442
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APPLICATION NUMBER: PCT/
FTI.ING DATE: 22-SEP-1994
                                                                                                                     CLASSIFICATION: 435
                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 LVLAEFFAPWCGHCKALAP-KY-----EQAATELKEKNIPLVKVDCTEEEALCR 95
                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGAKDSPVEYEGSRTVEDLANFVKENG-KHKVDALEVDPKKEQESGD 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGE 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L--FYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMY 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESIGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAED 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQGVE-----GYPTLKIFRGLDAVK--PYQGARQTEAIVSYMVKQSL-PAVSPVTPENLE 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEFYAPWCGHCKALAPKYEELASLYKDIPEVTIAKID-ATANDV--PDSITGFPTIKLF
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                                                           24-SEP-1993
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                     PCT/JP94/01572
                                                                                                                                                         US/08/627,907A
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Patent No. 5879664
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INFORMATION FOR SEQ
SEQUENCE CHARACTER
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TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                     REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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NAME: HALEY Jr., James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194
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                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                        STREET: 405 Le:
CITY: New York
                                                     TELEPHONE:
                                                                                                                                                                                    FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVENLP 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-----FKKFISDKDASIVGFFDDSFSEAHSEFLKAASNLRD---NYRFAHTNVESLV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LELTDDNFESRISDTGSAGLMLVEFFAPWCGHCKRLAPEYEAAATRLKG--IVPLAKVDC
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                                                                                                                          Lambiris, Elias
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                                      212-878-9655
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                                                       212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                               No. 58796640 No. 5879664disk of No. 5879664th Lexington Avenue, 64th Floor
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                       ID NO:
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22.6%;
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Pred. No. 9.7e-07;
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Patent No. 6346244
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                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                    REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Fungal Protein Disulfide Isomerase NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                   APPLICATION NUMBER: US 08/557,122 FILING DATE: 11-DEC-1995 ATTORNEY, AGENT INFORMATION:
                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSYAGMLGTKDLLKF 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 VAETVERDRKRKLPLE-LTVELTEETENATVMASDSIVL-FYAGWQAVSMAFLQSYIDVA 415
                                  TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
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                                                                                                                    NAME: Lambiris, Elias REGISTRATION NUMBER:
                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LASSVFAQQEAVAPEDSAVVKLATDSFNEYIQSHDLVLAEFFAPWCGHCKNMAPEYVKAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CWLNL--KNTPVGRGIL 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DVFEKWLQVEALPYFGEI------DGSVFAQYVESGLPLGYLFYNDEEELEEYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEMFPE-ITVENLPSYFRLQKPLLILFSDGTVNPQYKKAILTL-----VKQKYLDSFTP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDYDFVSAENADDDFKLSIYLPSAMDEPVVYNGKKAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGYVITGIYSEEDVLLLSTKYAASL--PALLLARHTEGKIESIPLASTHAQDIVQIITDA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --MIKQSQPA-VAVVADLPAYLANETFVTPVIVQSGKIDADFNATF-----YSMANKHF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETLV-EKNITLAQIDCTENQDLCMEHNIPGFPSLKIFKNRDVNNSIDYEGPRTAEAIVQF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66;
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530 amino acids
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                                                                                                                    33,728
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                                                                                                      3980.204-US
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Pred. No. 2.
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: E
US-09-262-666-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Applicati
Patent No. 5879664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                       TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 400
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 --MIKQSQPA-VAVVADLPAYLANETFVTPVIVQSGKIDADFNATF-----YSMANKHF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 IQLNRISYPVNITSIQEAEEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYL 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 CWLNL--KNTPVGRGIL 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 LLEMFPE-ITVENLPSYFRLQKPLLILFSDGTVNPQYKKAILTL-----VKQKYLDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 NDYDFVSAENADDDFKLSTYLPSAMDEPVVYNGKKAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 VKLKGTSTMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGE--NPVSYAGMLGTKDLLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 LFTELAKKN----RGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 --DVFEKWLQVEALPYFGEI------DGSVFAQYVESGLPLGYLFYNDEEELEEYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 KGYVITGIYSEEDVLLLSTKYAASL--PALLLARHTEGKIESIPLASTHAQDIVQIITDA
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LASSVFAQQEAVAPEDSAVVKLATDSFNEYIQSHDLVLAEFFAPWCGHCKNMAPEYVKAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
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                                                                                                                                           TELEPHONE:
                      TOPOLOGY:
                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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Similarity 20.8%;
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                                                     amino acid
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                                                                      521 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 58796640 No. 5879664d1sk of No. 5879664th America, 5 Lexington Avenue, 64th Floor
                      linear
                                                                                                                                               212-867-0123
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 peptide
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                                                                                                                                                                                  3980
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Pred. No. 2.1e-05;
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                                                                                                                                                                                  204 - US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126;
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US-08-557-122A-32

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646 CWLNL--KNTPVGRGIL 660
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275 LFTELAKKN----RGLM 287
                                                                                                                               134 --MIKQSQPA-VAVVADLPAYLANETEVTPVIVQSGKIDADENATE-----YSMANKHE 184
                                                                                                                                                                                                                                                                 358 VAETVFRDRKRKLPLE-LTVELTEETFNATVMASDSIVL-FYAGWQAVSMAFLQSYIDVA 415
                                                                                      592 LLEMFPE-ITVENLPSYFRLQKPLLILFSDGTVNPQYKKAILTL-----VKQKYLDSFTP 645
                                                                                                                                                                                                                       474 IQLNRISYPVNITSIQEAEEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYL 533
                                                                 226 -- DVFEKWLQVEALPYFGEI ------ DGSVFAQYVESGLPLGYLFYNDEEELEEYKP 274
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Search completed: March 13, 2003, 17:15:00 Job time : 23 secs

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Title:
Perfect score:
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            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
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length: 2000000000
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Match
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Gapop 10.0 ,
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Listing first 45 summaries
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: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
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: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
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: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *
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Sequence 8, Appl
Sequence 86, Appli
Sequence 869, Appl
Sequence 1661, Ap
Sequence 15, Appl
Sequence 436, App
Sequence 90, Appl
Sequence 74, Appl
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LENGTH: 807
TYPE: PRT
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Matches
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ALIGNMENTS

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; ORGANISM: Homo sapiens US-09-847-046-2
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APPLICANT: Hevezi, Peter
APPLICANT: Hack, David
APPLICANT: Gish, Kurt C.
APPLICANT: Wilson, Keith E.
APPLICANT: Wilson, Keith E.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF PROSTATE AND/OR BREAST CANCER,
TITLE OF INVENTION: MODULATORS
TITLE OF INVENTION: MODULATORS
FILE REFERENCE: A-69199-1/DJB/JJD/AMS
CURRENT APPLICATION NUMBER: US/09/847,046
CURRENT FILING DATE: 2001-12-08
PRIOR APPLICATION NUMBER: US 09/733,288
PRIOR APPLICATION NUMBER: US 09/787,576
PRIOR APPLICATION NUMBER: US 09/687,576
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
    121
                                                                            61 VAKVNCVKEEISRYCGKEKDLMKAYLFKGNILLREFPTDTLFDVNAIVAHVLFALLFSEV
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US-10-108-605-51
                                                                         TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LA FILE REFERENCE: 31133B

FILE REFERENCE: 31133B

CURRENT APPLICATION NUMBER: US/10/108,605

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US/761,142

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/176,418

PRIOR FILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 361

SOFTWARE: PATENTIN VET: 2.1
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APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
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  Query Match
                                                                   SEQ ID NO 51
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                                  ORGANISM: Drosophila
                                              TYPE: PRT
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Sequence 8, Application US/09759010

Patent No. US20010034042A1

REMERAL INFORMATION:

APPLICANT: Srivastava, Pramod K.

TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK

TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS

FILE REFERENCE: 8449-135

CURRENT APPLICATION NUMBER: US/09/759,010

CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 515

TYPE: PRT

COGGANISM: Homo sapiens

US-09-759-010-8
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                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                         Query Match
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CURRENT FILING DATE: 2001-08-10
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
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PRIOR FILING DATE: 2000-03-08
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LOCATION: (7)
OTHER INFORMATION: Xaa equals any
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TKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVENLP 605
                                                                                                                                         ADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEA 491
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                                  E----FKKFISDKDASIVGFFDDSFSEAHSEFLKAASNLRD---NYRFAHTNVESLV
                                                                     EEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLS 551
                                                                                                       TANTITCNKYGVSGYPTLKIFRDGEEAGAYDGPRTADGIVS--HLKKQAGPASVPLRTEE 182
                                                                                                                                                                             LELTDDNFESRISDTGSAGLMLVEFFAPWCGHCKRLAPEYEAAATRLKG--IVPLAKVDC 124
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SEQ ID NO 1661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA101
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NAME/KEY: SITE
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AGMLGTKD---LLKFIQ 475
                                   KQLEPVYNSLAKKYKGQKGLVIAKMD-ATANDVPSDRYKVEGFPTIYFAPSGDKKNPVKF
                                                                      MAFLQSYIDVAVKLKGTSTMLLTRINCADWSDV-CTKQNVTEFPIIKMYKKGE--NPVSY 461
                                                                                                       VTAFKKGKLKPVIKSQPVPKNNKGPVKVVV---GKTFDSIVMDPKKDVLIEFYAPWCGHC
                                                                                                                                        VFRDRKRKL-----
                                                                                                                                                                                                            NVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDMEGPDIDVQDDEVAET
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Pred. No.
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Mismatches 211;
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Sequence 15, Application US/09788657
Patent No. US20020123149A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,336
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 769
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Best Local Similarity
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TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: Yeast
FILE REFERENCE: 01107.00097
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APPLICANT: Sass, Philip
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-----LLARHTEGKIESIPLASTHAQDIVQIITDALLEMFPEITVE---
                                  LI-LYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLSTKYAASLPAL
                                                                                                        DYKVPSIADDEKNALPISKDG------YIRVPKERVNVNLTSIKKLREKVDDSIHRE
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Grasso, Luigi
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19.2%; Pred. No. 0.
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APPLICANT: BENSON, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LI
FILE REFERENCE: 21011.475C10
CURRENT APPLICATION UNMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 436
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.1%; Score 129; DB 9; L Best Local Similarity 20.4%; Pred. No. 0.011; Matches 79; Conservative 54; Mismatches 134;
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APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
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                                      ---PLPPLPLLVL-----VNLHSGGQ 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAHSD
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SKYSVRGYPTLLLFRGGKKVSEHSGGR
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                                                                                 NTFDDTIAEGI-TFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAEVDCTAERNIC
                                                                                                                          GTVNPQYKKAILTLVK-----QKYLDSFTPCW--LNLKNTPVGRGILRAYFD-----
                                                                                                                                                                  RDLESLREYVESQLQRTETGATETVTPSEAPVLAAEPE-----ADKGTVLALTE
                                                                                                                                                                                                                                                                                            EDFSE----AGNYLKGYVITGIYSEEDVLLLSTKYAASLPALLLARHTEGK-----
                                                                                                                                                                                                                                                                                                                                     PELKQGLYELSASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGK
                                                                                                                                                                                                                                                                                                                                                                                                                    VCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPV--TPEPEVEPPSA 148
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LENGTH: 396
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                  GENERAL INFORMATION:
APPLICANT: Ashkenaz
                                                                                                                    Sequence 90, Application US/09978295A Patent No. US20020156006A1
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Best Local
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                                 APPLICANT:
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CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.4
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APPLICANT:
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                                                                   APPLICANT:
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                                                                                    Ashkenazi, Avi
                 Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Indirias, Carol Yoseph
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Ferrara, Napoleon
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Fling, Steven P.
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/65250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR ETLING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
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                                  PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
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PRIOR FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/078910 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/078939
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR APPLICATION NUMBER: 60/078004
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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CURRENT FILING DATE: 2001-10-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
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                                                                            APPLICATION NUMBER: 60/079786
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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                                                RDLESLREYVESQLQRTETGATETVTPS----EAPVL-----AAEPEADKGTVLALTEN
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PRIOR APPLICATION NUMBER: 09/918585
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con, David L.
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OR FILING DATE: 1998-03-27
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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FILING DATE: 1997-11-13
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Botstein, David
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OR APPLICATION NUMBER: 60/078004

OR APPLICATION NUMBER: 60/078806

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Baker Kevin P.
                                                       Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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              Williams, P. Mickey Wood, William I.
                                             Tumas,
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Hillan, Kenneth J
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llarity 20.0%; Pred. No. 0.015;
Conservative 52; Mismatches 140;
                                                                                                                                                                                                                                                                                        Wei-Qiang
                                                                                                                       James;
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                                            Daniel
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 Secreted and
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085689
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APPLICATION NUMBER: 60/085580
FILING DATE: 1998-05-15
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APPLICATION NUMBER:
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085579
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                                                                                                                                                                                                                                                                                                                                                         KYLD----
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                                                                                                                                                                                                                                                                                              -PLPPLPLLVL-----VNLHSGGQ
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Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                            Application US/09978189
                                                        Filvaroff, Ellen
                                                                                                   Desnoyers, Luc
                                                                                                                    Botstein, David
                                                                                       Eaton, Dan
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Pred. No. 0.019
52; Mismatches
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DR APPLICATION NUMBER: 60/083495
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083496
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083499
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083545
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FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392

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1998-04-27 1998-04-23

60/083322 60/083336

FILING DATE: 1998-0 APPLICATION NUMBER:

APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21

FILING DATE: 1998-04-22 APPLICATION NUMBER:

60/082700

60/082804

FILING DATE: 1998-04-29

FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0

FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838

1998-04-15

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60/082568

60/082704

FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0

.998-04-15

998-04-15

FILING DATE:

1998-04-15

60/081952 60/081819 60/081817

APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955

APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:

998-04-08

60/081195 60/081203

1998-04-08

R APPLICATION NUMBER: 60/083559
R FILING DATE: 1998-04-29
R PRESIDENT NUMBER: 60/083500
R FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083742
DR FILING DATE: 1998-04-30

APPLICATION NUMBER: 60/083558

1998-04-29

FILING DATE:

PR FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-07
PR FILING DATE: 1998-05-07
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/08
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PR APPLICATION NUMBER: 60/08
PR FILING DATE: 1998-05-07
PR FILING DATE: 1998-05-07

APPLICATION NUMBER: FILING DATE: 1998-01 APPLICATION NUMBER:

1998-05-06

60/084441

APPLICATION NUMBER:

1998-05-07 NUMBER: 60/084639 1998-05-07

60/084640

APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06

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CURRENT FILING PRIOR APPLICATION PRIOR FILING DA
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OR APPLICATION NUMBER: 60/06250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064249
OR PILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/06364
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/07636
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/07763
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/07764
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/07764
OR APPLICATION NUMBER: 60/07764
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/077804
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/07804
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/07893
OR APPLICATION NUMBER: 60/07893
OR APPLICATION NUMBER: 60/07893
OR APPLICATION NUMBER: 60/07993
OR APPLICATION NUMBER: 60/07963
OR APPLICATION NUMBER: 60/07964
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/07964
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079664
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OR APPLICATION NUMBER: 60/079663
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OR APPLICATION NUMBER: 60/079768
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OR FILING DATE: 1998-03-37
OR APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 09/918585
FILING DATE: 2001-07-30
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A
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P. Mickey
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DR APPLICATION NUMBER: 60/081819
DR APPLICATION NUMBER: 60/081819
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081838
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/082568
DR FILING DATE: 1998-04-21
DR APPLICATION NUMBER: 60/082569
DR FILING DATE: 1998-04-21
DR APPLICATION NUMBER: 60/082704
DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082704
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DR APPLICATION NUMBER: 60/082700
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DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082797
DR APPLICATION NUMBER: 60/082797
DR APPLICATION NUMBER: 60/082797
DR APPLICATION NUMBER: 60/08333
DR APPLICATION NUMBER: 60/08336
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083392
DR APPLICATION NUMBER: 60/083495
DR APPLICATION NUMBER: 60/083
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DR APPLICATION NUMBER: 60/081071
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DR APPLICATION NUMBER: 60/081195
DR FILING DATE: 1998-04-08
DR FILING DATE: 1998-04-09
DR APPLICATION NUMBER: 60/081203
DR FILING DATE: 1998-04-09
DR FILING DATE: 1998-04-09
DR FILING DATE: 1998-04-05
DR APPLICATION NUMBER: 60/081955
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FILING DATE: 1998-04-01
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1998-04-15
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APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/085700
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YSVRGYPTLLLFRGGKKVSEHSGGR 415
                                 -PLPPLPLLVL-----VNLHSGGQ 683
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20.0%; Pred. No. 0.015;
ative 52; Mismatches 140;
                                                                                                     -----SFTPCW--LNLKNTPVGRGILRAYFD------
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US-10-176-758-74
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US-10-174-590-74
                                                             Sequence 74, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application removed -
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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TYPE: PRT
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Goddard, Audrey
Godowski, Paul J.
Desnoyers, Luc
Goddard, Audrey
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APPLICANT: Wood William I.

APPLICANT: Wood William I.

APPLICANT: Zhang,Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C104

CURRENT APPLICATION NUMBER: US/10/176,758

CURRENT APPLICATION NUMBER: US/10/176,758

CURRENT FILING DATE: 2002-06-21

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NO 74

LENGTH: 432

TYPE: PRT

GRANISM: Homo Sapien

US-10-176-758-74
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APPLICANT:
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391 YSVRGYPTLLLFRGGKKVSEHSGGR 415
                                         666 -PLPPLPLLVL-----VNLHSGGQ 683
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                                                                                  331 NFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAEVDCTAERNICSK 390
                                                                                                                                    638 KYLD-----
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Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                -----SFTPCW--LNLKNTPVGRGILRAYFD------
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Search completed: March 13, 2003, 17:18:06 Job time : 21 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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protein disulfide	SSSMSI	L	509	3.1	127.5	44
protein disulfide-	S68280	N	489	3.1	127.5	43
hypothetical prote	T23055	N	488	3.1	127.5	42
hypothetical prote	E86349	N	977	3.1	128	41
hypothetical prote	T47655	N	2149	3.1	128.5	40
protein disulfide-	S71863	N	485	3.2	130.5	39
protein disulfide-	T37630	N	363	3.2	130.5	38
inner layer protei	P1XRSR	ш	1088	3.2	131	37
hypothetical prote	T25887	N	574	3.2	131.5	36
probable protein o	T09614	N	364	3.2	131.5	S
reticulocyte-bindi	A42771	Ŋ	2829	3.2	132	34
hypothetical prote	T32636	N	572	3.2	133	ω ω
probable protein d	T00437	Ŋ	361	3.2	133	32
protein disulfide-	ISMSER	ᆫ	638	3.2	133.5	<u>ω</u>
endoplasmic reticu	S06318	Ν	584	3.2	133.5	30

ALIGNMENTS

O.; Yamada, Y.; Hirai, M.; disulfide isomerase

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28-May-1999

A; Molecule type: protein
A; Molecule type: protein
A; Residues: 21-46;55-66;77-110;115-124;171-187;207-212;330-339;353-374;395-404;416-43
C; Comment: This enzyme catalyzes thiol-protein-disulfide interchange in vitro, with v
C; Superfamily: protein disulfide-isomerase; thioredoxin homology
C; Keywords: 91ycoprotein; intramolecular oxidoreductase; isomerase
F;1-20, Domain: signal sequence #status predicted <SIG>
F;21-505/Product: protein disulfide-isomerase #status predicted <MAT>
F;29-112/Domain: thioredoxin homology <TXI>
F;39-112/Domain: thioredoxin homology <TXI> F;105/Binding site: carbohydrate (Asn) (covalent) #status predicted A; Accession: PC2200 A; Molecule type: mRNA A; Residues: 1-505 < KAJ> F;363-450/Domain: thioredoxin homology <TX2> A;Cross-references: GB:S74296; NID:g712822; PIDN:AAC60578.1; PID:g71282: 15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY Local Similarity les 112; Conserv DSLEV----NIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEEIQEDEDNDM D-YMSAGIPLAYIFAETAEERKELSDKLKPIAEAQRGVINFGTIDAKAFGAHAGNLNLKT TVHLQLGLPLVFIVSQQA---EDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAEDPQQVS LEEFKKADKA-----VLVAYVDASDKASSEVFTQVAEKLRDNYPFGSSSDAALAEAEGV LEDLQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGTTYQFVLTTEIALLESIGS --EETDLCQQHGVEGYPTLKVFRGLDNVSPYKGQRKAAAITSYMIKQSLPAVSEVTK-DN CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN LVLAEFFAPWCGHCKALAP------EYEEAATTLKEKNIKLAKVDCT-----Conservative ----AIVLYKDFDEGKAVFSEKFEVEAIEKFAKTGATPLIGEIG--PETYS 4.5%; ----79; Score 185; DB 2; Pred. No. 0.00023; 9; Mismatches 213 -TYEADRRTAEW--VAWRLLG-KAGVLLLLR --Length 505; Indels 108; Gaps 191 137 125 74 239 245 185 80 22;

QY 613 PLLILESDGTVNPQYKKAILTLVKQKYLDSFTPCWLNLKNTPVGRGILRAYFDPLP 668	OY 555AASLPALLLARHTEGKIESIPLASTHAQDIVQIITDALLEMFPEITVENLPSYFRLOK 612 Db 304 SSPVKLQVMLFSKADDFOKLAQPLEDIARKFKSKLMFIYVDITNENLAM 352	Qy 529 554	QY 488 IQEAEBYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSE 528	Qy 428 RINCADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITS 487 : : : : : : : : : : : : : : : : : : :	Qy 369 KLPLELTVELTEETFNATVMASDSIVLFYAGWQAVSMAFLQSVIDVAVKLKGT-STMLLT 427 ::	Qy 317 LVLHDVDLIISHVENNMHIEEIQEDEDNDMEGPDIDVQDDEVAETVFRDRKR 368	Query Match 4.4%; Score 182; DB 2; Length 546; Best Local Similarity 20.9%; Pred. No. 0.00041; Matches 111; Conservative 93; Mismatches 180; Indels 148; Gaps 25;	ry A STC GE	n, X; Liu, S.X; Liu, Z.A.; Lurs, J.S.; Maiti, R.; Marziali, ley, D.; Sakano, H. Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, raser, C.M.; Venter, J.C.; Davis, R.W. ysis of chromosome 1 of the plant Arabidopsis.	A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K Hughes, B.; Huizar, L. 16-820, 2000	hypothetical protein F19K6.17 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession. F0K6K2	QY 462 AGMLGTKDLLKFIQLNRISYPVNITSIQEAEE 493 Db 448 SGSRTVEDLIKFIAENG-KYKAAISEDAEE 476	Qy 407 FLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTKQNVTEEPIIKMYKKGENPVSY 461	354 EGPVTVVAKNYNEIVLDDTK	Ov 347 EGPDIDVODDEVAETVFRDRKKKLPLELTVELTEETFNATVWASDSIVLFYAGWOAVSWA 406
RESULT 4 \$34275 protein disulfide-isomerase homolog precursor - fluke (Schistosoma mansoni)	QY 736AATSQRGTRKVPKCMKETDVQENDK 760 1	QY 679 HSGGQVFAFPSDQAIIEENLVLMLKKLEAGLENHITILPAQEWKPPLPAYDFLSMID 735	- QY 626 QYKKAILTLVKQKYLDSFTPCWLNLKNTPVGRGILRAYFDPLPPLPLLVLVNL 678 : : : : : : : : : : : : : : : : : : : : : :	QY 566 HTEGKIESIPLASTHAQDIVQIITDALLEMEPEITVENLPSYERLQKPLLILESDGTVNP 625	QY 518 TMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLSTKYAASLPALLLAR 565	QY 458 PVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGELYKDLILYSSVSVLGLFSP 517	Qy 399 GWQAVSMAFLQSYIDVAVKLKGT-STMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGEN 457	Query Match 4.2%; Score 172.5; DB 2; Length 664; Best Local Similarity 19.4%; Pred. No. 0.0024; Matches 87; Conservative 90; Mismatches 175; Indels 97; Gaps 1 Qy 345 DMEGP-DIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVL-FYA 398	A;Introns: 43/2; 110/2; 631/3 A;Introns: 43/2; 110/2; 631/3 C;Superfamily: protein disulfide-isomerase; thioredoxin homology C;Keywords: intramolecular oxidoreductase; isomerase E;90.170/Domain: thioredoxin homology <tx1> F;201-285/Domain: thioredoxin homology <tx2> F;553-640/Domain: thioredoxin homology <tx3></tx3></tx2></tx1>	e ty	K;Favello, A.D. submitted to the EMBL Data Library, May 1993 A;Description: Sequence of the C. elegans cosmid C14B9. A;Reference number: S44617 A;Reference number: S44617	or 4 cf 10		709 LENHITTLPAQEWKPPLPAYDFLSMIDAATSQRGTRKVPKCMKETDVQENDK 760	Db 413 DNENASIVTVVGKTFDGLVLNSRENVLLEVHTPWCVNCEALSKOIEKLAKHFKG 466

	y 736AATSQRGTRKVPKCMKETDVQENDK 760	Дy
735 515	679 HSGGQVFAFPSDQAIIEENLVLWLKKLEAGLENHITILPAQEWKPPLPAYDFLSMID	Дb
678 466	626 QYKKAILTLVKQKYLDSFTPCWLNLKNTPVGRGILRAYFDPLPPLPLLVLVNL : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	DP QA
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565 382	518 TMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLSTKYAASLPALLLAR	Db Qy
517 329	458 PVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGELYKDLILYSSVSVLGLFSP	당 성
457 279	399 GWQAVSMAFLQSYIDVAVKLKGT-STMLLTRINCADWSDVCTKONVTEFPIIKMYKKGEN 	Db Qy
398 219	345 DMEGP-DIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVL-FYA :	P 64
aps 17;	Query Match 4.2%; Score 172.5; DB 2; Length 664; Best Local Similarity 19.4%; Pred. No. 0.0024; Matches 87; Conservative 90; Mismatches 175; Indels 97; Ga	7 m c
	Introns: 43/2; 110/2; 631/3 ;Superfamily: protein disulfide-isomerase; thioredoxin homology ;Keywords: intramolecular oxidoreductase; isomerase ;90-170/Domain: thioredoxin homology <tx1> ;201-285/Domain: thioredoxin homology <tx2> ;533-640/Domain: thioredoxin homology <tx3></tx3></tx2></tx1>	55.00
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	tion:	sul A; I A; I
-1999	ion 12-May-1995 #text_change 16-J	RCCCZ
legans	protein disulfide-isomerase (EC 5.3.4.1) - Caenorhabditis e	RES S44
	y 709 LENHITILPAQEWKPPLPAYDFLSMIDAATSQRGTRKVPKCMKETDVQENDK 760 : : : : :	ОУ
708 466	669 PLPLLVLVNLHSGGQVFAFPSDQAIIEENLVLWLKKLEAG : : : : : :	ОУ

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protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor - human k;Alternate names: ER-60 proteinase C;Specles: Homo sapiens (man) C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 21-Jan-2000 C;Accession: JC5704; G02888 R;Urade, R;Oda, T; Ito, H.; Moriyama, T.; Utsumi, S.; Kito, M. J. Biochem. 122, 834-842, 1997 A;Title: Functions of characteristic Cys-Gly-His-Cys (CGHC) and Gln-Glu-Asp-Leu A;Reference number: JC5704; MUID:98060510; PMID:9399589 A;Accession: JC5704
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C; Superfamily: protein disulfide-isomerase; thioredoxin homology C; Keywords: duplication; endoplasmic reticulum; redox-active disuriation; endoplasmic reticulum; redox-active disuriation; endoplasmic predicted <SIG>F; 1-15/Domain: signal sequence #status predicted <SIG>F; 31-115/Domain: thioredoxin homology <TXI>F; 369-452/Domain: thioredoxin homology <TXI>F; 369-482/Region: endoplasmic reticulum retention signal F; 52-55, 391-394/Disulfide bonds: redox-active #status predicted F; 125-142/Disulfide bonds: #status predicted
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C;Date: 22-Nov-1993 #sequence_
C;Accession: S34275
R;Finken, M.; Sobek, A.; Symmo
submitted to the EMBL Data Lib
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                                                                                                                                                                                                                                                                                                                                   VCTKQ----NVTEFPIIKMY-KKGENPVSYAGMLGTKDLLKFIQ
                                                                                                                                                                                                                                                                                                                                                                               VGKNYNDVVKDKSKDVFVKLYAPWCGHCKALAPVWDELGETFKNSDTVIAK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRIIELGEETTKYKPDTNDYSVSAMSDFVQRTI--DGKVK-PFLMSEEIPSDQTGAVKVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LONIENALKGKANI-IESYVR---AIGIPEHRAVM----EAGFVYG-----TTYQFVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKHG-EKGYPTLKFFR-----NEQPIDFLGERDSDAIVN---WCLRKSKPSVEYIDSLDS 141
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                                                                                                                                                                                                                                                                                               ATVNEVEDLKVTSFPTLKFYPKNSEEVIDYTGDRSFEALKKFVE
                                                                                                                                                                                                                                                                                                                                                                                                                      TEETFNATV--MASDSIVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSD 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDSLEVNIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%;
22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library, June
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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une 1993
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                                           (QEDL)
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A;Reference number: S68279; MUID:96257756; PMID:8687406 A;Accession: S68279
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C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S68363; S78215; S68279
R;Bourdi, M.; Demady, D.; Martin, J.L.; Jabbour, S.K.; Martin, B.M.; George, Arch. Biochem. Biophys. 323, 397-403, 1995
                                                                                                                                                                                                                               A;Accession: 5/04...
A;Molecule type: protein
A:Molecule type: protein
                                                                                                                                                                                R;Koivunen, P.; Helaakoski, T.; Ann
Biochem. J. 316, 599-605, 1996
A;Title: ERp60 does not substitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S68363; MUID: 96063616; A; Accession: S68363
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A; Molecule type: mRNA
A; Residues: 1-505 <KOI>
                                                                          A; Status: not compared with
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: U42068; NID: g1147738; PIDN: AAC50331.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-505 <BOU>
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F;384-470/Domain: thioredoxin homology <TXN>
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A; Residues: 1-505 < UR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA cloning and Baculovirus expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LIQGKDLLIAYYDVDYEKNAKGSNYWRNRVMMVAKKFLDA
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22.68;
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                                                                          translation
                                                                                                                                                                                                                                                                  P.; Veijola, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMID:7487104
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F;1-24/Domain: signal sequence

C;Superfamily: protein disulfide-isomerase; thioredoxin homology C;Keywords: endoplasmic reticulum; intramolecular oxidoreductase

intramolecular oxidoreductase;

isomerase;

redox-ac

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
S57942
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C;Keywords: intramolecular oxidoreductase;
F;33-116/Domain: thioredoxin homology <TX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X89449; NID:g899148; PIDN:CAA61619.1; PID:g899149 C;Superfamily: protein disulfide-isomerase; thioredoxin homology C;Keywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-515 <MAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.6
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Best Local :
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                                                                                                                                                                  142
                                                                                                                                                                                                          126
240 ETYSG-YIGAGVPLAYIFA-ETKEEREKYTEDFKPIAQKHKGAINIATIDAKMFGAHAGN
                                          242
                                                                                    196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492
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                                                                                                                                                                                                                                                                                                                                                                     15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 LELTDDNFESRISDTGSAGLMLVEFFAPWCGHCKRLAPEYEAAATRLKG--IVPLAKVDC
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                                          QQVSTVHLQLGLPLVFIVSQQATYEADRRTAEW----
                                                                                                                                                                                                      LEDLQNIENALKGKANIIFSYVRAIGIPEHRAVMEAGFVYGTTYQFVLTTEIALLESIGS
                                                                                                                                                                                                                                                                                      CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN 125
                                                                                                                                                                                                                                              ----DLCRSQGVEGYPTLKIFRGVDSSKPYQGARQTESIVSYMIKQSLPAVSSVNE-EN
                                                                                                                                                                                                                                                                                                                               LVLAEFFAPWCGHCKALAP-KY------EEAATELKAKNIPLVKVDCTAEE----
                                                                                EQPSIV-LYKDFDEKKAVYDGEIEQEA------IHSWVKSASTPLVGEIG--P
                                                                                                                        EDVEYAHLY -- FFHCKLVLD--LTQQCRRTLMEQPLTTLNIHLFIKTMKAPLLTEVAEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVENLP
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                                                                                                                                                                LEEIKTMDKI-----VVIGYIPSDDQETYQAFEKYAESQRDNYLFAATDDAAIAKSEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LIQGKDLLIAYYDVDYEKNAKGSNYWRNRVMMVAKKFLDA 293
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 169.5; Ub ... Score No. 0.0025;
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.rematches 127;
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                                                                                                                                                                                                                                                                                                                                                                                                               Indels 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 515;
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                                          VAWRLLG-KAGV
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    297
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protein disulfide-isomerase

(EC

5.3.4.1) ER60

precursor

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RESULT 10
S63994
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revis
C;Accession: S55507
R;Charnock-Jones, D.
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-488/Product: ER60 protease #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                 A; Residues: 1-505 <HIR>
A; Residues: 1-505 <HIR>
C; Superfamily: protein disulfide-isomerase; thioredoxin homology C; Keywords: endoplasmic reticulum; intramolecular oxidoreductase. F; 33-118/Domain: thioredoxin homology <TXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-505 <HIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: S63994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hirano, N.; Shibasaki, F.; Sakai, R.; Tanaka, T.; Nishida, Eur. J. Blochem. 234, 336-342, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Date: 20-Jul-1996
C; Accession: S63994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor - human
N;Alternate names: glucose-regulated protein GRP58
C;Species: Homo sapiens (man)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 13-Jun-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-505 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: Cloning, ex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title:
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                             376 VELTEETFNATVMASDS----IVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $63994; MUID:96096758;
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22.6%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compared with conceptual translation
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                                                                                                                         59;
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                                                                                                                    Score 166.5; DB
Pred. No. 0.0038;
9; Mismatches 12
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                                                                                                                                                                                                           DB 2;
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J. Biol. Chem. 200, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 24333, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 2433, 243
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                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-82, V',84-142,'S',144,146-167,'E',169-225,'V',227-457,'S',459-505,'EADA
A; Cross-references: EMBL:X52313; NID:g3948; PIDN:CAA36550.1; PID:g3949
A; Cross-references: EMBL:X52313; NID:g3948; PIDN:CAA36550.1; PID:g3949
                                                                                                          R;Guenther, R.; Braeuer, C.; Janetzky, B.;
J. Biol. Chem. 266, 24557-24563, 1991
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A; Residues: 1-522 <LAM>
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                                                                                                                                           TKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVENLP
---LIQGKDLLIAYYDVDYEKDAKGSNYWRNRVMMVAKKFLDA
                                           SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS
                                                                                             NEYDDNGEGIILFRPSHLTNKFEYKTVAYTEQKMTSGKIKKFIQENIFGICPHMTEDNKD
                                                                                                                                                                                                                                           EEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLS
                                                                                                                                                                                                                                                                                            TANTNTCNKYGVSGYPTLKIFRDGEEAGAYDGPRTADGIVS--HLKKQAGPASVPLRTEE
                                                                                                                                                                                                                                                                                                                                       ADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEA 491
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                                                                                                                                                                                              ----FKKFISDKDASIVGFFDDSFSEAHSEFLKAASNLRD---NYRFAHTNVESLV
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A;Molecule type: protein
A;Residues: 99-112;'X',185-193;211-217;'X',233-237,'X',239;284-286,'X',288-298;309-31
R;LaMantia, M.; Miura, T.; Tachikawa, H.; Kaplan, H.A.; Lennarz, W.J.; Mizunaga, T.
Proc. Natl. Acad. Sci. U.S.A. 88, 4453-4457, 1991
A;Title: Glycosylation site binding protein and protein disulfide isomerase are ident
A;Reference number: A39376; MUID:91239586; PMID:1840696
A;Accession: A39376 A; Title: Molecular structure of a yeast gene, A; Reference number: JX0182; MUID:92105067; PM C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000 C;Accession: JX0182; PS0224; A39376; S15050; JS0634; S40913; A41713; S19372; A;Cross-references: GB:D00842; A;Accession: PS0224 A; Molecule type: DNA A; Residues: 1-522 < TAC> A; Accession: JX0182 R;Tachikawa, H.; Miura, T.; Ka J. Biochem. 110, 306-313, 1991 N; Alternate names: protein YCL043c; protein C; Species: Saccharomyces cerevisiae protein disulfide-isomerase (EC Katakura, Y.; Mizunaga, NID: g218506; 5.3.4.1) precursor - yeast (Saccharomyces cerevisiae) 43c; protein YCL313; S-S rearrangase; thioredoxin-rela PMID:1761527 PIDN:BAA00723.1; PID:g218507 protein disulfide isomer

A; Molecule type: DNA A; Residues: 1-113,'R',115-505,'EADAEAEA',506-522 A; Cross-references: EMBL:X54535; NID:g4119; PIDN A:Title: Protein disulfide isomerase is essential for viability A;Reference number: JS0634; MUID:92104510; PMID:1761235 A;Accession: JS0634 A;Cross-references: EMBL:x57712; NID:g4801; PIDN:CAA40883.1; PID:g4802 R;Farguhar, R.; Honey, N.; Murant, S.J.; Bossier, P.; Schultz, L.; Mon A; Molecule type: DNA A; Residues: 1-522 <SCH> A;Cross-references: GB:M62815 R;Scherens, B.; Dubois, E.; M A; Accession: S15050 A; Title: Determination of the sequence of the yeast YCL313 gene A; Reference number: S15050; MUID:91289690; PMID:2063627 185-193, 1991 81-89, 1991 Messenguy, <FAR> localized in Saccharomyces Montogomery, D.; 9 chromoso cere

(F)

NID: g4119; PIDN: CAA38402.1;

PID: 94120

gene is essential PMID:1761554

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I.M.; Lehle, L.;

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reast to 5//-586, 1992

A;Title: The complete sequence of a 9,543 bp segment on the left arm A;Reference number: $25347; MUID:92397595; PMID:1523890

A;Reference number: $25349

A;Recession: $25349

A;Recession: $25349

A;Rocessidues: 1-522 <SC2>

A;Coross-references: EMBL:X59720; EMBL:$43845; EMBL:$49180; EMBL:$580

C;Genetics:

A;Gene: $GD:PDI1; MFP1; TRG1; MIPS:YCL043c

A;Cross-references: $GD:$0000548; MIPS:YCL043c

A;Gene: $GD:PDI1; MFP1; TRG1; MIPS:YCL043c

A;Genetics: $GD:PDI1; MFP1; MIPS:YCL043c

A;Genetics: $GD:PDI1; MFP1; MIPS:YCL043c

A;Genetics: $GD:PDI1; MIPS:YCL043c

A;Genetics: $GD:PDI1; MIPS:YCL043c

A;Genetics: $G
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A; Molecula
A; Residue;
A; Cross-ra
R; Dubois,
protein disulfide-isomerase (EC 5.3.4.1) ER60 precu
N;Alternate names: endoplasmic reticulum protein ER
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 27-Jun-1994
C;Accession: A28807; A43050; A43051; A40095
R;Bennett, C.F.; Balcarek, J.M.; Varrichio, A.; Cro
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A;Cross-references: GB:M76982; NID:g173023; PIDN:AAA35169.1; PID:g173024
A;Robols, E.; Pierard, A.; Gigot, D.; Glansdorff, N.; Messenguy, F.; Scherens, B.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19367
A;Reference number: S19367
A;Accession: S19372
A;Ancession: S19372
A;Molecule type: DNA
A;Residues: 1-522 <DUBb
A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42373.1; PID:g5320; GSPDB:GN00003
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Yeast 8, 577-586, 1992
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Residues: 1-82,'V'
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Pred. No. 0.
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A;Cross references: GB:X12355; NID:g56904; PIDN:CAA30916.1; PID:g569)
R;Martin, J.L.; Punford, N.R.; LaRosa, A.C.; Martin, B.M.; Gonzaga, I
Biochem. Biophys. Res. Commun. 178, 679-685, 1991
A;Title: A metabolite of halothane covalently binds to an endoplasmin, A;Reference number: A43050; MUID:91315499; PMID:1650195
A;Accession: A43050
A;Molecule type: protein
A;Residues: 25-37;95-104;130-138;274-279;366-378;426-450;482-495 <MAI
R;Urade, R; Nasu, M; Moriyama, T; Wada, K; Kito, M.
J. Biol. Chem. 267, 15152-15159, 1992
A;Title: Protein degradation by the phosphoinositide-specific phospho A;Reference number: A43051; MUID:92340568; PMID:1321829
A;Accession: A43051
A;Molecule type: protein
A;Residues: 25-34;173-194;432-459 <URA>
R;Mobbs, C.V.; Fink, G; Pfaff, D.W.
Science 247, 1477-1479, 1990
protein disulfide-isomerase (EC N; Alternate names: ER60 proteina C; Species: Mus musculus (house m C; Date: 25-Dec-1994 #sequence_re C; Accession: S41661 R; Mazzarella, R.A.; Marcus, N.;
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A;Reference number: A40095
A;Recession: A40095
A;Molecule type: protein
A;Residues: 26-43 <MOB>
C:Comment: ER60 may be part of a complex capable of catalyzing cl
C:Comment: ER60 protease does not appear to be a cytoplasmic 1-ph
C:Comment: ER60 protease does not appear to be a cytoplasmic 1-ph
C:Comment: ER60 protease does not appear to be a cytoplasmic 1-ph
C:Comment: ER60 protease does not appear to be a cytoplasmic 1-ph
C:Comment: ER60 protease does not appear to be a cytoplasmic 1-ph
C:Comment: ER60 protein disulfide-isomerase; thioredoxin homology
C:Keywords: duplication; endoplasmic reticulum; intramolecular ox
C:Superfamily: signal sequence #status predicted <SIC>
E:C-52-56A/Domain: Signal sequence #status predicted <SIC>
E:C-52
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A;Title: Molecular cloning;
A;Reference number: A28807;
A;Accession: A28807
A;Molecule type: mRNA
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33-118/Domain: thioredoxin homology <TXI>
501-504/Region: endoplasmic reticulum retention signal #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E---
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(house mouse)
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                                                                                                                                                                         5.3.4.1)
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                                                                        #text_change 17-Mar-1999
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Gonzaga, H.M.S.;
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C:Superfamily: protein disulfide-isomerase; thioredoxin homology c:Keywords: intramolecular oxidoreductase; isomerase; multifunctional F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-517/Product: protein disulfide-isomerase #status predicted <MAT>
F:59-66/Domain: redox-active #status predicted <REAL>
F:59-66/Domain: redox-active #status predicted <REAL>
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Biochem. Biophys. Res. Commun. 281, 1176-118, 2001
A;Title: Characterization of a gene encoding a Pichia pastoris
A;Reference number: JC7623; MUID:21139750; PMID:11243858
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F;383-469/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Biochem. Biophys. 308, 454-460, 1994
A;Title: ERp61 is GRP58, a stress-inducible luminal endoplasmic reticulum protein, A;Reference number: S41661; MUID:94153092; PMID:8109975
A;Accession: S41661
                                                                                                                                                                                                                                                              F;401-408/Domain:
                                                                                                                                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain GS115
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:AJ302014
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-517 <WAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JC7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Accession: JC7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein disulfide-isomerase (EC 5.3.4.1) precursor -
C;Species: Pichia pastoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
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KELCQGYEIKGYPTLKVFHGEVEVPSDYQGQRQSQSIVSYMLKQSLPPVSEINATKDLDD
                                   SDVCTKQNVTEFPIIKMYK-KGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEE 493
                                                                            VKLTEATFESFITSNPHVLAEFFAPWCGHCKKLGPELVSAAEILKDNEQVKIAQIDCTEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein disulfide-isomerase homolog F28P10.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 22-Oct-1999
C;Accession: T06724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.
A;Experimental source: cultivar Columbia; BAC clone F28F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-566 < QUE>
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Best Local Similarity 20.5
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                                                                                                                                                                                                                                                                                                                                                         CTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                      TEETFNATV-MASDSIVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDV
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                                                                              EVAKSFKGKFVFVYVQMDNEDYGEAVSGFFGVTGAAPKVLVYTGNEDMRKFILDG-----
                                                                                                                                                                                              DFSEA----GNYLKGYVITGIYSEEDVLLLS-TKYAAS---
                                                                                                                                                                                                                                                                                                                    AQKYETQGFPTVFLFVDGEMRKTYEGERTKDGIVTWLKKKASPSIHNITTKEEAERVLSA
                                                                                                                                                                                                                                                                                                                                                                                                 TKDNFTEFVGNNSFAMVEFYAPWCGACQALTPEYAAAATELKGLAA--LAKIDATEEGDL
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                                     PEITVENLPSYFRLQKPLLILFSDGTVNPQYK----
                                                                                                                                                           EEEKLARFDGNFTKTAIAEFVSANKVPLVINFTREGASLIFESSVKNQANESEKHLPTLR
                                                                                                                                                                                                                                       EPKLYFGFLNSLYGSESEELAAASRLEDDLSFYQTASPDIAKLFEIETQYKRPALYLLKK
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KTLAEDFLADKLKPFYKSDPLPENNDGDVKVIVGNNFDEIVLDES
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1; Mismatches
                                                                                                                                                                                                                                                                             --LYKDLILYSSVS--VLGLFS-----
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Pred. No. 0.074;
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Gaps

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		Search completed: March 13, 2003, 17:14:33 Job time : 25 secs	Qy 638 KYLDSFTPCWLNLKNTPVGRGIL-'RAYFDPLPPLPLLVLVNLH 679
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Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
  Length DB
  Gapext 0.5
            PDI_RAT
PDI_BOVIN
PDI_BOVIN
EUG1_YEAST
PDA4_MOUSE
PDA6_ARATH
RBP1_PLAVB
PDA6_MEDSA
RRP0_ROTS1
Y659_PASMU
PD1_HAEIN
PD1_MOUSE
PD1_MOUSE
                                                                                                                                                                                              PDA3_MOUSE
PDI_YEAST
BS2_TRYBB
PDI1_SCHPO
PDA4_RAT
PDA4_HUMAN
ER60_SCHMA
MLH1_YEAST
YBA4_YEAST
PDI_RABIT
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PDI_DROME
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PDI_ASPOR
PDA4_CAEEL
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P38659
P38659
P38659
P38659
P37723
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 Q9cmz1
P25655
P09102
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P09103
Q9xi01
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                          4 saccharomyc
5 oryctolagus
5 rattus norv
7 homo sapien
7 bos taurus
4 saccharomyc
                                                                                                                                                                                                                                                                                                                             8 aspergillus
9 caenorhabdi
1 homo sapien
0 aspergillus
5 rattus norv
          a mus musculu
a arabidopsis
b plasmodium
medicago sa
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pasteurella
saccharomyc
gallus gall
haemophilus
mus musculu
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8 schistosoma
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drosophila
bos taurus
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PDI_HUMIN
ID PDI_HUMIN
AC P55059;
Query Match
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						-	
homo sapien	094822	2294 HUMAN	_	1818	2.8	116	5
homo sapien	Q9y376	MO25_HUMAN	<u> </u>	341	2.8	116	44
bovine rota	P21615	RRPO_ROTBU	ب	1088	2.9	118.5	43
homo sapien	076041	NEBL_HUMAN	Н	1014	2.9	118.5	42
homo sapien	Q14554	PDA5_HUMAN	_	519	2.9	118.5	41
schizosacch	013811	PDI2_SCHPO	_	359	2.9	119.5	40
homo sapien	293009	UBP7_HUMAN	μ.	1102	2.9	120	39
h a-kinase	Q99996	AKA9_HUMAN	۳	3911	2.9	121.5	38
bovine rota	P17468	RRPO_ROTBR	_	1088	2.9	121.5	37
mycoplasma	P75350	UVRC_MYCPN	ب	586	2.9	122	36
b gramicidi	P14688	GRSB_BACBR	_	4451	3.0	122.5	35
bacillus th	P07130	C3AA_BACTT	Н	644	3.0	123	34

ALIGNMENTS

STANDARD;

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.
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MEDLINE-20196006; PubMed-10731132;
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RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
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RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Correll J.H., Gu Z., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Ra Harris K.F., Zaveri J.S., Shanders R.D.C., Scheeler F., Shen H.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yilskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Yang A.H., Wang S., Yang Y., Jane Q.A.,
RA Yang A.H., Wang S., Yang Y., Sheng L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
-i- TISSUE SPECIFICITY: EXPRESSED IN ALL HEAD AND BODY TISSUES.
-i- DEVELOPMENTAL STAGE: UBIQUITOUSLY EXPRESSED DURING DEVELOPMENT
-i- SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0014002; Pdi.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein disulfide isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERP60) (58 kDa microsomal protein) (P58) (ERP57).
  This
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                   secretory form and inducible
                                                                                                                                                                                                                                                                 Yazaki Y., Takenawa T., Hirai H.;
"Molecular cloning of the human glucose-regulated protein ERp57/GRP58, a thiol-dependent reductase. Identification
                                                                                                                                                                                                                                                                                                                  Hirano N., Shibasaki F., Sakai R., Tanaka T., Nishida
Yazaki Y., Takenawa T., Hirai H.;
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96096758; PubMed=8529662;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                       transformation.";
Eur. J. Biochem. 234:336-342(1995).
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                                         CAUTION: WAS ORIGINALLY THOUGHT TO BE A PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE TYPE I (PHOSPHOLIPASE C-ALPHA).
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                                                                                                               SUBCELLULAR LOCATION: Endoplasmic reticulum.lumen
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                                                                                                             Lee B., Yamada O., Kitamoto K., Takahashi K.;
Submitted (JUN-1996) to the EMBL/GenBank/DDB databases.
-i- FUNCTION: PARTICIPATES IN THE FOLDING OF PROTEINS CC
DISULFIDE BONDS, MAY BE INVOLVED IN GLYCOSYLATION, I
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TIGREAMS; TIGR01130; ER.PDI_fam; 1.
TIGREAMS; TIGR01130; ER.PDI_fam; 2.
PROSITE; PS00194; THIOREDOXIN; 2.
Redox-active center; Isomerase; Endoplasmic reticulum; Repeat;
SIGNAL 1 24 BY SIMILARITY.
                                                  HYDROXYLATION AND TRIGLYCERIDE TRANSFER (BY SIMILARITY) -I- CATALYTIC ACTIVITY: Rearrangement of both intrachain an
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PROSITE; PS00194; THIOREDOXIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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  STANDARD
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61
396
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19.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 172.5; DB 1;
Pred. No. 0.00061;
7; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
REVENT SECRETION FROM ER (POTENTIAL)
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PROTEIN DISULFIDE ISOMERASE.
    PRT;
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    618
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Query Match
Best Local S
Matches 87
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DISULFID
DISULFID
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Bonfield J., Burton J., Connell M., Copsey T., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeer
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                  Endop1
                                                                                                                                                                                                                        WormPep; C14B9.2; CE00073.
InterPro; IPR000886; ER_target.
InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 3.
PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. Then use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                   PRINTS; PR00421; THIOREDOXIN.
TIGREAMS; TIGR01126; pdi_dom; 3.
TIGREAMS; TIGR01130; ER_PDI_fam; 1
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00194; THIOREDOXIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: NOT KNOWN.
-i- CATALYTIC ACTIVITY: Rearrangement of both interchain disulfide bonds in proteins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable protein disulfide isomerase A4 precursor
                                                                                                                                                                                                                                                                                                                   EMBL; L15188; AAM22024.1; PIR; S44756; S44756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N. STRAIN-Bristol N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Rhabditidae; Pelode:
                                                     SEQUENCE
                                                                             DISULFID
                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                           MEROPS; C17.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: CONTAINS :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94150718; PubMed=7906398;
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 87; Conservative
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                                                      ĂA;
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              4.2%;
19.4%;
                                                                                                                                             Isomerase; Redox-active center;
; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Endoplasmic reticulum lumen 3 THIOREDOXIN DOMAINS.
                                                      X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oda; Chromadorea; Caenorhabditis.
  90;
              Score
Pred.
                                                                             PROBABLE PROTEIN DISULFIDE IS
REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
                                                                 PREVENT
                                                                                                                                  POTENTIAL.
                                                     1DC0207A71444220
Mismatches
              172.5; DB
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                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
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P30101; 014255; 013453; 09UMU7;
01-APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein disulfide isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERP60) (58 kDa microsomal protein) (p58) (ERp57)
(58 kDa glucose regulated protein).

PDIA3 OR GRP58 OR ERP60.
MEDINIE-96063016; PubMed=7487104;
MEDINIE-96063016; PubMed=7487104;
Bourdi M., Demady D., Martin J.L., Jabbour S.K., Martin B George J.W., Pohl L.R.;
"cDNA cloning and baculovirus expression of the human live endoplasmic reticulum P58: characterization as a protein isomerase isoform, but not as a protease or a carnitine
                                                                                                                                                                                                                                                  Kito
                                                                                                                                                                                                                                                                                                                   Charnock-Jones D.;
Submitted (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirano N., Shibasaki F., Katon H.
Yazaki Y., Takenawa T., Hirai H.;
                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholipase
alpha.";
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phospholipase C-alpha: proposal of redesignation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibasaki F., Katoh H.,
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Catarrhini;
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Proteomics 2:212-223(2002)
-!- CATALYTIC ACTIVITY: Re
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                                                                                                                                                                                  Harris R.A., Yang A., Stein Parekh R., Waterfield M.D.,
                                                                                                                                                                                                      MEDLINE=21829512; pubMed=11840567;
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon carci
MEDLINE=97295306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simpson R.J., Dorow D.S.;
"Two-dimensional electrophoretic analysis of human proteins: mapping of proteins that bind to the SH3 lineage kinase MLK2.";
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"Structures of the human gene for the protein disulfide isomerase-
related polypeptide ERp60 and a processed gene and assignment of t-
genes to 15q15 and 1q21.";
                                                                                                                                               Zvelebil M.J.;
"Cluster analysis of an extensive |
"Cluster analysis of an extensive |
                                                                                                                                                                                                                          TISSUE-Breast
                                                                                                                                                                                                                                                           Electrophoresis
                                                                                                                                                                                                                                                                        protein database
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                                                                                                                                                                                                                                                                                                           Rasmussen H.H., van Damme
                                                                                                                                                                                                                                                                                                                     TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93162045; PubMed=1286669;
Hochstrasser D.F., Frutiger S., Paquet N.
Pasquali C., Sanchez J.-C., Tissot J.-D.,
Appel R.D., Hughes G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymph;
Strausberg R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rasmussen R.K., Ji H.,
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                                SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity)
MASS SPECTROMETRY: MW=54265.22; METHOD=MALDI.
SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
CAUTION: WAS ORIGINALLY THOUGHT TO BE A PHOSPHATIDYLINOSITOL-4,5-
BISPHOSPHATE PHOSPHODIESTERASE TYPE I (PHOSPHOLIPASE C-ALPHA).
                                                                                 SUBCELLULAR LOCATION:
                                                                                                         interchain disulfide
          SWISS-PROT entry
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          is copyright. It is produced through a collaboration
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e M.J.,
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PHCI-2DPAGE; P30101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).

A -> G (IN REF. 3).

A -> Y (IN REF. 1).

D -> Y (IN REF. 1).

Q -> P (IN REF. 2).

E -> G (IN REF. 2).

N -> G (IN REF. 1).

D -> G (IN REF. 1).

D -> G (IN REF. 1).

D -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 169.5; DB Pred. No. 0.00093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.00
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN DISULFIDE ISOMERASE A3. REDOX-ACTIVE (BY SIMILARITY). REDOX-ACTIVE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREVENT SECRETION FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529E5B6692D0D7E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
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VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY

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RESULT 7
PDI_ASPNG
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               Query Match
Best Local
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1)
SEQUENCE FROM N.A.
STRAIN-CBS 120.49 / N400;
STRAIN-CBS 120.49 / Nather D.B.;
MEDLINE-97174110; PubMed-9021130;
MISOLATION and Characterisation of a gene
"Isolation and characterisation of a gene
"Isolation and characterisation of a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDI_ASPNG
Q12730;
Q1-NOV-1997 (
01-NOV-1997 (
30-MAY-2000)
                                                                              DISULFID DISULFID
                                                                 SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Protein disulfide isomerase precursor (EC 5.3.4.1)
PDIA OR PDII.
                                                                                                                                             TIGRRAMS; TIGRO1126; pd1_dom; 2.
TIGRAMS; TIGRO1130; ER_PD1_fam;
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00194; THIOREDOXIN; 2.
                                                                                                                                                                                                                                                    EMBL; X98797; CAA67332.1; -. EMBL; X89449; CAA61619.1; -. HSSP; P07237; IMEK.
                                                     SEQUENCE
                                                                                                                     Redox-active SIGNAL
                                                                                                                                                                                                  InterPro; IPR000886; ER_target.
InterPro; IPR00063; Thiored.
Pfam: PF00085; thiored; 3:
PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                        entities requires
or send an email t
                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as modified and this statement is not r\varepsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-NRRL
Malpricht S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eurotiales; Trichocomaceae;
                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Rearrangement of both interchain disulfide bonds in proteins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: PARTICIPATES IN THE FOLDING OF PROTEINS CONTAINING DISULFIDE BONDS, MAY BE INVOLVED IN GLYCOSYLATION, PROLYL HYDROXYLATION AND TRIGLYCERIDE TRANSFER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606
                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                       structures
                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LIQGKDLLIAYYDVDYEKNAKGSNYWRNRVMMVAKKFLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYFRLQ-KPLLILFSD-----GTVNPQYKKAILTLVKQKYLDS
                                                                                                                                                                                                                                                                                                        s requires a license agreement (S an email to license@isb-sib.ch).
               Similarity
                                                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics
                                                                   21
54
389
512
  Conservative
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                                                                                                                                   center;
                                                      AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                  ter; Isomerase; Endoplasmic reticulum; Re
20 POTENTIAL.
515 PROTEIN DISULFIDE ISOMERASE.
57 REDOX-ACTIVE (BY SIMILARITY)
392 REDOX-ACTIVE (BY SIMILARITY)
392 PREVENT SECRETION FROM ER (P
515 PREVENT SECRETION FROM ER (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascomycota; Pezizomycocomaceae; mitosporic
             20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                            Endoplasmic reticulum lumen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                               THIOREDOXIN DOMAINS.
  ; 68
                                                                                                                                                                                                                                                                                                                                   is not removed.
Pred. No. 0.00
9; Mismatches
                                                     REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
PREVENT SECRETION FROM ER (PO
; 2B0058B788400AD9 CRC64;
                           Score
                                                                                                          PROTEIN DISULFIDE ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pezizomycotina; Eurotiomy itosporic Trichocomaceae;
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            169
No.
                                                                                                                                                                                                                                                                                                                                              long
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ger.";
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                                                                 (POTENTIAL).
                                                                                                                                   Repeat;
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MRI outstation -
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein disulfide isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-50) (ERp60) (58 kDa microsomal protein) (p58) (ERp57)
       Martin J.L., Pumford N.R., Larosa A.C., Mart Beaven M.A., Pohl L.R.;
Beaven behave a finite of halothane covalently binds reticulum protein that is highly homologous phosphatiaylinositol-specific phospholipase
                                                                                                                                      SEQUENCE FROM N.A.
Kito M., Urade R.;
Kito M. of novel microsomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDA3_
                                                                                                       PARTIAL SEQUENCE.
                                                                                                                                  Proc. Jpn.
                                                                                                                                                                                                 phosphoinositide-specific phospholipase
                                                                                                                                                                                                                           MEDLINE=88288403; PubMed=3398923;
Bennett C.F., Balcarek J.M., Varrichio A.,
"Molecular cloning and complete amino-acid
                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                    PDIA3 OR GRP58
                                                                                                                                                                                                                                                                                                                                                                                                                                                P11598;
                                                                            MEDLINE-91315499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGFPTLRLYPAGAKDSPIEYSGSRTVEDLANFVKENG-KHNVDALNVASEETQEGGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGKEKDLMKAYLFKGNILLREF-----PTDTLFDVNAIVAHVLFALL--FSEVKYITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: |: | :| |:| || || LVLAEFFAPWCGHCKALAP-KY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEFPIIKMYKKG--ENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEEYLSGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APWCGHCKALAPKYDELAALY - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSDVCTK-------QNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDEDNDMEGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEETFNATVMASDSIVL--FY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNLDSQKFPAFAIQDPAKNAKYPYDQAKELNADEVEKFI----QDVLDGKVEPSIKSEPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLLRDSLEVNIPQD----ANVVFKRAEE--GVPVEFLVLHDVDLIISHVENNMHIEEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQPSIV-LYKDFDEKKAVYDGEIEQEA------IHSWVKSASTPLVGEIG--P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DLCRSQGVEGYPTLKIFRGVDSSKPYQGARQTESIVSYMIKQSLPAVSSVNE-EN
                                                                                                                                Acad.,
                                                                                                                                                                                                                                                                  N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                              PubMed=1650195;
ord N.R., Larosa
                                                                                                                                  B
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                                                                                                                                cysteine pr
. Biol. Sci.
                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                               proteases.";
ci. 71:189-192(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EEAATELKAKNIPLVKVDCTAEE----
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                                                                                                                                                                                                               C. ";
                                                               Martin
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                                                                                                                                                                                                                        Crooke S.
         to
C-alpha
                                   to an endoplasmic
                                                               В.м.,
                                                                                                                                                                                                                              of
                                                              Gonzaga H.
                                                                                                                                                                                                                                                                                                           Murinae; Rattus
                                                                                                                                                                                                                            form-I
                                                                                                                                                                                                                                                                                                                                                                              (ERp57)
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DISULFID DISULFID

25 57 406

PROTEIN DISULFIDE ISOMERASE A3 REDOX-ACTIVE (BY SIMILARITY). REDOX-ACTIVE (BY SIMILARITY). PREVENT SECRETION FROM ER

CHAIN

CONFLICT

MRFSCLALLPGVA

1).

MPSAALRCSRAWR

Ή

YB)

SIMILARITY).

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EMBL; X12355;
EMBL; D63378;
PIR; A28807; A
                                                                                                       PRINTS: PRO0421; THIOREDOXIN.
TIGRFAMS: TIGR01126; pdi_dom; 2.
TIGRFAMS: TIGR01130; ER_PDI_fam;
PROSITE: PS00194; THIOREDOXIN; 2
                                                                                                                                        InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Protein degradation by the phosphoinositide-specific C-alpha family from rat liver endoplasmic reticulum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification and characterization of a new isozyme of thiol:protein-disulfide oxidoreductase from rat hepatic microsomes. Relationship of this isozyme to cytosolic phosphatidylinositol-specific phospholipase C form lA.";
                                                                                              Redox-active
                                                                                                                                                                               MEROPS; C17.001;
                                                                                                                                                                                             HSSP; P07237; 1MEK.
                                                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                          modified and this statement is not removed
                                                                                                                                                                                                                                                                                                        use
                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Inhibition by acidic phospholipids of protease, a novel cysteine protease, of FEBS Lett. 312:83-86(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBITION BY PHOSPHOLIPIDS.
MEDLINE=93050170; PubMed=1330685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Urade R., Nasu M., Moriyama T., Wada K.,
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MEDLINE=90208308; PubMed=2181662;
Mobbs C.V., Fink G., Pfaff D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-34; 174-193; 433-446 AND MEDLINE=92340568; PubMed=1321829;
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"HIP-70: a protein induced by es
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SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A PHOSPHATIDYL-
INOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE TYPE I (PHOSPHOLI
C-ALPHA) THEN WAS THOUGHT (REF.6 AND REF.7) TO BE A THIOL
PROTEASE.
                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
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ENZYME REGULATION:
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                                                                                                                                                                                                                  5; CAA30916.1;
8; BAA09695.1;
; A28807.
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                                                                                               Isomerase;
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Best Local
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CONFLICT
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SEQUENCE
                                                                                Merrick B.A., Wichter L.L., Patterson R.M., He C., Sell Tidentification of the two isoforms of phospholipase C. dividing murine fibroblasts by protein microsequencing Biochem. Arch. 9:335-340(1993).
                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein disulfide isomerase A3 precursor (EC isomerase ER-60) (ERp60) (58 kDa microsomal p. PDIA3 OR GRPSB OR ERP60) OR ERP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDA3_MOUSE P27773;
                                                                                                                                                  TISSUE=Fibroblast;
                                                                                                                                                                                   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selki "Separation and sequencing of familiar and novel murine using preparative two-dimensional gel electrophoresis."; Electrophoresis 15:735-745(1994).
                                                                                                                                                                                                                                    TISSUE=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
                                                                                                                                                                                                                                                                                   Hempel W.M., Defranco A.L.; "Expression of phospholipase C i J. Immunol. 146:3713-3720(1991).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-91237072; PubMed=2033248;
                                                                                                                                                             SEQUENCE OF 25-41,
                                                                                                                                                                                                                                                             SEQUENCE OF 25-41.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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STRUCTURES.
SUBCELLULAR LOCATION: Endoplasmic reticulum
PTM: PHOSPHORYLATED.
SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
CAUTION: WAS ORIGINALLY THOUGHT TO BE A PHC
                                                                            interchain disulfide
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Rodentia;
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IKKFIQESI -> SRSLFRF
F -> L (IN REF. 2).
EAC7F0C0BD4F1471 (
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Sciurognathi; Muridae;
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(PHOSPHOLIPASE C-ALPHA).
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Murinae; Mus
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Best Local :
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DISULFID
SITE
SEQUENCE FROM N.A.; AND PARTIAL S STRAIR-X2180-1A, and TM5; MEDLIXE-92105067; PubMed-1761527; Tachikawa H., Miura T., Katakura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO1126; pdi_dom; 2.
TIGREAMS; TIGRO1130; ER_PDI_fam; 1.
TIGREAMS; TIGRO1130; ER_PDI_fam; 2.
RedOx-active center; Isomerase; End
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-2DPAGE; P27773;
MGD; MGI:95834; Grp58
InterPro; IPR000063;
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                  related glycoprotein 1).
PDI1 OR MFP1 OR TRG1 OR YCL043C
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                                                                                                                                               Saccharomycetales;
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                                                                                          EMBL;
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"Protein disulfide isomerase
Saccharomyces cerevisiae.";
Gene 108:81-89(1991).
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J. Biol. Chem. 266:24557-24563(1991).
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Lehle L., Kuentzel H.;
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Scherens B., Dubois E., Messenguy
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Chromosome III. Homology with the
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J. Biochem. 110:306-313(1991).
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SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS
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91239586; PubMed=1840696;
Miura T., Tachikawa
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for cell viability in yeast.";
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TIGREAMS; TIGR01130; ER_DDI_fam;
PROSITE; PS00014; ER_TARGET; 1.
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of rat protein-disulfide isomerase and
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Cronin A., Davis P., Feltwell T., Fraser A.,
COllins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Squares S., Stevens K.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Woestl D., Hilbert H.,
RA Gerry M., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gerger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Ra Geffeau A., Cadieu E., Dreano S., Gloux S., Lehaure V., Motter S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shalowski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415: 871. The Follows Contantony PROLYL
LYGERT M., The Follows Contantony PROLYL
LYGERT M.
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15-JUN-2002 (Rel. 41, Last annotation update)
Putative protein disulfide isomerase CIF5.02;
SPACIF5.02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21848401; PubMed-11859360;
Wood V., Gwilliam R., Rajandream M
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                                                                                                                                                                                                                                                                                                                  DISULFIDE BONDS, MAY BE INVOLVED IN GLYCOSYLATION, PROI HYDROXYLATION AND TRIGLYCERIDE TRANSFER (BY SIMILARITY) CATALYTIC ACTIVITY: Rearrangement of both intrachain an interchain disulfide bonds in proteins to form the nati
                                                                                                                                                                                                                   SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Endoplasmic reticulum
                                                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGRVEPTIKSLPV----PEVETVDGKTTIVAKTMQK 361
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PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00194; THIOREDOXIN; 2.
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                                                                                                                                  ELTVELTEETFNATVM--ASDSIVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRIN
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                                                                                ATE-NDISV--SISGFPTIMFFKANDKVNPVRYEGDRTLEDLSAFIDKHASFEPI
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N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict most by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00421; THIOREDOXIN.
TIGREAMS; TIGR01126; pdi_dom; 3.
TIGREAMS; TIGR01130; ER_PDI_fam; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Liver; MEDLINE-93238767; PubMed-8477750; Van P.N., Rupp K., Lämpen A., Soe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M86870;
HSSP; P07237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redox-active center; Isomerase; Endoplasmic reticulum; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein disulfide isomerase A4 precursor (EC (ERP72) (Calcium-binding protein 2) (CaBP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "CaBP2
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                                  184
                                                                     291
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                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                   15 VIMCIFYMPTVNSLPELSPQKYFSTLQPGLEELNEAVRPLQDYGISVAKVNCVKEEISRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURES.
SUBCELLULAR LOCATION: Endoplasmic reticulum lum INDUCTION: UPON GLUCOSE STARVATION, AS WELL AS TUNICAMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: O-GLYCOSYLATED.
SIMILARITY: CONTAINS 3 THIOREDOXIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biochem 213:789-795(1993)
CATALYTIC ACTIVITY: Rearrangem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interchain disulfide
                                                                                                                                                                                                               IILVEFYAPWCGHCKKLAPE-----YEKAAKELSKRSPP-----IPLAKVDAT---
                                GSEDVEYAHLYFFHCKLVL------DLTQQCRRTLMEQPLTT--LNIHLFIKTMKAPLL-
                                                                                                                                         -- EQTDLAKRFDVSGYPTLKIFRKGRPFDYNGPREKYGIVDYMVEQSGPPSKEILT----
                                                                                                                                                                            CGKEKDLMKAYLFKGNILLREFPTDTLFDVN-----AIVAHVLFALLFSEVKYITNLED
                                                                                                      LQNIENALK-GKANIIFSYVRAIGIPEHRAVMEAGFVYGTTYQF--VLTTEIA--LLESI
                                                                   LKQVQEFLKDGDDVVILGVFQGVGDPGYLQYQDAANTLREDYKFHHTFSTEIAKFLKVSL
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115; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00014; ER_TARGET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00194; THIOREDOXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000886; ER_target. IPR000063; Thiored.
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72806 MW;
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KLVLMQPEKFQSKYEPRMHVMDVQGSTEASAIKDYVVKHDLPLVG
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e bonds in proteir
                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                                                                                                                                             Pred. No. 0.006; Mismatches
                                                                                                                                                                                                                                                                                                                  Score 142;
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Sciurognathi;
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AS TREATMENT
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P13667;
                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ-!- CATALYTIC ACTIVITY: Rearrangement of both interchain disulfide bonds in proteins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lung, and Muscle;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91161636; PubMed=2002068; Huang S.-H., Tomich J.M., Wu H., Jo J. Biol. Chem. 266:5353-5353(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang S.-H., Tomich J.M., Wu H., Jong A., "Human deoxycytidine kinase. Sequence of cexpression in cell lines with and without J. Biol. Chem. 264:14762-14768(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-MAY-1991 (Rel. 18, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Protein disulfide isomerase A4 precurs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
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                                                                                                                                          send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Endoplasmic reticulum SIMILARITY: CONTAINS 3 THIOREDOXIN DOMAINS. CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO E
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  BC000425; AAH00425.1; -. BC001928; AAH01928.1; -. BC006344; AAH06344.1; -. BC011754; AAH11754.1; -.
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                                                                                              J05016; AAA58460.1;
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Matches 74
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01-FEB-1995
01-FEB-1995
30-MAY-2000
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01-FEB-1995 (Rel. 31, Last sequal 30-MAY-2000 (Rel. 39, Last announce probable protein disulfide ison
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MEDLINE-94359529; pubMed-8078516; Finken M., Sobek A., Symmons P., Finken M., Sobet A., Symmons P., Sobet A., Symmons P., Sobet A., Symmons P., Symmons P., Symmons P., Sobet A., Symmons P., Sobet A., Symmons P., Symmons
                                                             SEQUENCE FROM N.A. STRAIN-Liberian;
                                                                                                                                        Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
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TIGRFAMS; TIGRO1130; ER_PDI_fam;
PROSITE; PSO0014; ER_TAMEET; 1.
PROSITE; PS00194; THIOREDOXIN; 3.
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HSSP; P07237; 1MEK.
MEROPS; C17.002; -.
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SITE
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Pfam; PF00085; thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
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TIGREAMS; TIGRO1130; ER_PDI_fam; 1.
TIGREAMS; TIGRO1130; ER_PDI_fam; 1.
PROSITE; PS00194; THIOREDOXIN; 2.
PROSITE; PS00194; Isomerase; Endoplasmic reticulum; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z22934; CAA80521.1; -. HSSP; P07237; 1MEK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structures.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
CAUTION: WAS ORIGINALLY THOUGHT TO BE A PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE TYPE I (PHOSPHOLIPASE C-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Biochem. Parasitol. 64:135-144(1994). CATALYTIC ACTIVITY: Rearrangement of both intrachain and interchain disulfide bonds in proteins to form the native
                                                                                              V--EFLVLHDVDLIISHVENNMHIEEIQEDEDNDMEGPDIDVQDDEVAETVFRDRKRKLP
                                                                                                                                                                                            KLVLDLTQQCRTTLMEQPLTTLNIHLF----IKTMKAPLLTEVAEDPQQVSTVHLQLGLPL
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                                                                                                                             VFAYSFADDFSYEISDYGIE------ADKLPAVVIQSKDKKYKLEKFSLD
                                                                                                                                                             VFIVS--QQATYEADRRTAEWVAWRLLGKAGVLLLLRDSLEVNIPQDANVVFKRAEEGVP
                                                                                                                                                                                                                                                                                                                                                                                                                         CGKEKDLMKAYLFKGNILLREFPTDTLF------DVNAIVAHVLFALLFSEVK 121
-----NEE-----KDVMVVFHAGWCGHCKNLMPKYEEAASKVKNEPNLVLAAMD-
                               LELTVELTEETFNATVMASDSIVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINC 431
                                                                 AFSDELNKFEDGLLTPHVKS----EPLPTDDSSAVK-KLVALNFDEIVN
                                                                                                                                                                                                                                                             PSDNELRVYLPKRLRTKFEDDFAVYKGELESNNIKDWIRKHGQGLVGYRSPSNTFYFENS
                                                                                                                                                                                                                                                                                                                           EVSTVSD----VENVLSDDKPTVFAFVKSSSDPLIKTFMALAKSMVDDAVFCHSHNNLFVT 186
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REDOX-ACTIVE (BY SIMILARITY).
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1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_nammal:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr:
13: sp_vertebr:
14: sp_unclass:
15: sp_archeap:
16: sp_bacteri:
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O3h9w7 homo sapien
O9cs82 mus musculu
O8r2w8 mus musculu
O74568 trichoderma
                                                                                 Q9c818 arabidopsis
Q9lw75 arabidopsis
O76945 fasciola he
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Q9CLY4
Q9YTK3
P93358

ALIGNMENTS

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Q26593 schistosoma
Q99166 mus musculu
Q91281 cricetulus
Q8r6n2 thermoaner
Q91815 fugu rubrip
Q9gph2 bombyx mori
Q9c1z8 pichia past
Q8vx13 arabidopsis

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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CDNA FLJ12501 fis, clone NT2RM2001681.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9H9W7;
                                                           SEQUENCE FROM N.A.
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su Isogai T., Ota T., Hayashi K., Sugano S., Aotsuka S., Yoshikawa Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO22563; BAB14101.1;
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; 
Mammalia; Eutheria;
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Catarrhini;
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RC MEDLINE-21085660; pubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Shai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hordsheit H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashtzaki Y.,
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Matches
                  "Functional annotation of a full Nature 409:685-690(2001).
EMBL; AK017582; BAB30819.1; -.
MGD; MGI:1917811; 5730420B22Rik.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
5730420B22RIK protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9CS82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9CS82
                                                                                                               Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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     354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Mouse)
     AA;
354
39924 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
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1; Mismatches
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     42B75F03910AEC75
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ches 0;
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     CRC64;
                                                                                            collection.";
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Query Match Best Local Sim Matches 274;

Similarity

34.48;

Conservative

34;

Pred. Score 1423;

No. 1

.3e-93;

27;

.18;

Gaps

DB 11;

Length

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RESULT
074568
ID 07
AC 07
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Best Local S
Matches 149
074568;
074568;
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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Submitted (APR-2002) to t
Submitted (APR-2002) to t
EMBL; BC027108; AAH27108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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                                                                                                                            SAELQPGDRSTARREPVEMLRIKRWNTANWPKDTQEPFHHDKEL
                                                                                                                                                 LVLMLKKLEAGLENHITILPAQEWKPPLPAYDFLSMIDAATSQRGTRKVPKCMKETDVQE
                                                                                                                                                                                                     LVLWLKHLQAGLENPITVLSAQEWKPPLPAFDFLNMMDAPTSQAPTKKVLECQKEAEVQE
                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 66.5
149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 AA;
(TrEMBLrel.
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              19.7%;
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Pred. No. 2e-5
35; Mismatches
Created)
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Best Local S
Matches 111
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InterPro; IPRO00063; Thiored.
pfam; PF00085; thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
TIGREAMS; TIGRO1130; ER_PDI_fam; 1.
TIGREAMS; TIGRO1126; pdi_dom; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
PROSITE; PS000194; THIOREDOXIN; 1.
ISOMETASE; Redox-active center; Signal.
SIGNAL 2.0
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO1. Gen. Genet. 262:35-45(1999).
EMBL; AJ222773; CAA10978.1; -.
HSSP; P07237; IMEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Last sequence up 01-JUN-2002 (TrEMBLrel. 21, Last annotation Protein disulphide isomerase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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Saloheimo M.L.A., Lund M., Penttila M.E.;
"The protein disulphide isomerase gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypocreales; Hypocreaceae; Hypocrea.
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492
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nes 111; Conser
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                                                                                                                                                                                                                    LGK------AGVLLLLRDSLEV----NIPQDANVVFKRAEEGVPVEFLVLHD
                                                                                                                                                                                                                                                   AIRNFAQVAATPLVGEVG---PETYAGYMSAGIPLAYIFAETAEERENLAKTLKPVAEKY
                                                                                                                                                                                                                                                                NIHLFIKTMKAPLLTEVAEDPQQVSTVHLQLGLPLVFIVSQQATYEAD-RRTAEWVAWRL
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                                                                                                                                                                                                                                                                                                                                                                                                                   DCVEEADLCKEHGVEGYPTLKVFRGLDKVAPYTGPRKADGITSYMVKQSLPAVSALTKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCVKE-----
                           - PDEIQGFPTIKLYPAGDKKNPYTYSGARTVEDFIEFIKENGKYKAGVEIPAEPTEEAEA
                                                     TKQNVTEFPIIKMYKKGE--NPVSYAGMLGTKDLLKFIQLN-----RISYPVNITSIQEA
                                                                                                         TFNATVMASDSIVLFYAGWQAVSMAFLQSYIDVA---VKLKGTSTMLLTRINCADWSDVC
                                                                                                                                                                VDLIISHVENNMHIEEIQEDEDNDMEGPDIDVQDDEVAETVFRDRKRKLPLELTVELTEE
                                                                                                                                                                                            KGKINFATIDAKNFGSHAGNINLKTDKFPAFAIHDIEKNLKFPFDQSKEITEKDIAAFVD
                                                                                                                                                                                                                                                                                                                                 AGFVYGTTYQFVLTTEIALLESIGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTL
                                                                                                                                                                                                                                                                                                                                                              LEDFKTADKVVLVAYIAADDK - - ASNETFTALANELR - -
                                                                                                                                      -GFSSGKIEASIKSEPIPETQ----EGPVTVVVAHSYKDIVLDDKK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
502 AA;
                                                                                                                                                                                                                                                                                                       -DTYLFGGVNDAAVAE----AEGVKFP-----SIVLYKSFDEGKNVFSEKFDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                 DVLIEFYTPWCGHCKALAPKYDELASLYAKSDFKDKVVIAKVD-ATANDV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%;
20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 184.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN DISULPHIDE ISOMERASE; 159D6E787CAF3F02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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3.9e-05;
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

A Hunter J.L., Jonkins J., Johnson Hopson C., Khan S., Khaykin E.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Lin X., Liu S.X., Liu E.A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lingin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

A Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

N Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

"Sceneros and Anniverse of Anniverse T.G., Davis R.W.;

"Sceneros and Anniverse of Anniverse T.G., Davis R.W.;

"Sceneros and Anniverse of Anniverse T.G., Davis R.W.;
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Best Local Similarity
Matches 111; Conser
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EMBL; AC037424; AAG51554.1;
HSSP; P07237; 1MEK.
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MEDLINE=21016719; PubMed=11130712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
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InterPro; IPR000063; Thiored.
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                                        -----AGNYLKGY------VITGIYSEEDVL--LLSTKY------
                                                                          VDEAPREL - - DKYHTF - - - - -
                                                                                                                                                     KIDGDRYSKIASELEIKGFPTLLLFVNGTS-LTYNGGSSAEDIVIWVQKKTGAPIITLNT
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                                                                                                                                                                                                                                                                                                                                                                       Score 182; DB 10;
Pred. No. 0.00015;
3; Mismatches 180;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; agnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Dbj|BAA81871.1.
                                                                                                                                                                                                                                                                Pfam; PF00085; thiored; 3.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SEQUENCE 519 AA; 57859 MW; 40A4AB1C7CD2F123 CRC64;
                                                                                                                                                                                                                                                                                                                                EMBL; AB012247; BAF
HSSP; P07237; 1MEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato S., Nakamura Y., Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                      InterPro; IPR000886;
InterPro; IPR000063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
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ASTIKLDTVDEASGFLKKHHTFILGLFEKSEDSSGHDEFVKAASLDNEIQFVETSSIDVA
                        SYPVNITSIQEAEEYL----
                                                  IGSSVLMAKIDGERYSKVASQLEIKGFPTLLLFVNGTSQ-SYTGGFSSEEIVIWVQKKTG
                                                                       T-STMLLTRINCADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRI
                                                                                                                               VFRDRKRKLPLELTVELTEETFNATVMASDSI-VLFYAGWQAVSMAFLQSYIDVAVKLKG
                                                                                                                                                          KFSILFTFLLLLSFLIFVARSSDVAVEAGSEEELDDLEQLLAVDEQLQEERPEQQSEAET
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Last sequence update)
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                                                                                                                                                                                                            Score 178; DB
Pred. No. 0.00
02; Mismatches
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EMBL/GenBank/DDBJ
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Fasciola hepatica (Liver fluke).
Fasciola hepatica (Liver fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
NCBI_TaxID=6192;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protein disulphide isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO1130; ER_PDI_fam; 1.
TIGREAMS; TIGRO1126; pdi_dom; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00194; THIOREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and heterologous expression of Fasciola hepatic protein disulphide isomerase.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ225804; CAA12644.1;
HSSP; P07237; IMEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salazar M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       076945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     076945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000886; ER_target.
InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 3.
PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSOULD, CTIVE center.
Isomerase; Redox-active center.
047AF15027C872A4 CRC64;
                                                                                                                                                                                                                                                                                       376 VELTEETFNATVMASD-SIVLFYAGWQAVSMAFLQSYIDVAVKLKGT-STMLLTRINCAD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513
   149
                                                          493
                                                                                                                                                                            434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 INKE 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 LVFARIDASANEHPKLTVDDYPTILLYKTGE-----KENPLKLSTKSSAKDMAVL 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 LPSYFRLQKPLLILFSDGTVNPQYKKAILTLVKQKYLDSFTPCWLNLKNTPVG--RGILR 661
                                                                                                                    91
                                                                                                                                                                                                                                31 VELTEETFODEIKKKEFAMVMFYAPWCGHCKAMKPEYARAAAQLKEEGSDIMIAKVDATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRKE 772
                                                    EYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLST 552
                                                                                                                                                                         WSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITS-IQEAE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HI--TILPAQEWKPPLPAYDFLSMIDAATSQRGTRKVPKCMKETDVQENDKEQHEDKSA- 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYF--DPLPP---LPLLVLVNLHSGGQVFAFPSDQAII--EENLVLWLKKLE---AGLEN 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLARHTEG-----KIESIPLASTH------AQDIVQIITDALLEMFPEITVEN 603
QLVDKE---DIVV----
                                                                                                              HSKLAKSHNVTGYPTLKFYKSGV-WLDYTGGRQTKEIVHWIK-RKVSPAVSVLSTLSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYYKSQPIPDNQNASVVAVV-----GRTF----DEVVLRSSENVLLEVEKLSQHFKGFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LAMPFLTLFGIEDAKKTVVAAFDNNLNSKYLLESDPSPSNIEEFCFGLAHGTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYTKLTESNTVRVYSSPVKLQVMVFSKTDDFESLAQPLEDIARKFKSKLMLIYIDISNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLLFPNLKT------NNVFVGLVKTEAEKYTSYDGPCQAEKIVEFLNSNKFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLFSPTMKTAKEDFSEAGNYLKGYVIT------GIYSEEDVL--LLSTKYAASLPAL 561
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casais R., Diaz A., Martin J.M., Boga J.A., Parra F.; heterologous expression of Fasciola hepatica putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     4.2%; Score 176; DB 5;
23.2%; Pred. No. 0.00035;
Live 60; Mismatches 99
-----AVASVYDKYEFGFVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                           99;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 489;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                        Gaps
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190
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	MEGPDIDVQDDEVAETVFRDRKRKLPLELTVEL 378	Qy 338IQEDEDNDMEG	
	ż.	Db 287	
	RDSLEVNIPQDANVVFKRAEEGVPVEFLVLHDVDLIISHVENNMHIEE 337	Qy 289 LRDSLEVNIPQDA	
		Db 234 SEFSQKTA	
	LVFIVSQQATYEADRRTAEW	Qy 235 TEVAEDPQQVSTVHLQLGLP-	
		Db 198 PKIVLFKNFDENRVEYT	
	IGSEDVEYAHLYFFHCKLVLDLTQQCRRTLMEQPLTTLNIHLFIKTMKAPLL 234	Qy 175 TEIALLESIGSED	
	KANIAILGFIKDTDSLDLADFEKVADELDDAGFAIANSSEILTEYGITQT 197	Db 142 CKQFIDKAN	
	1	Oy 129 LONIENALKGKANI-IFSYVR-	
	LKFFRNEQPIDFLGERDSDAIVNWCLRKSKPSVEYIDSLDS 141	Db 91 LKHG-EKGYPTLKFFR-	
	GNILLREFPTDTLFDVNAIVAHV	Qy 73 RYCGKEKDLMKAY	
	HCKALAPEYSEAAKKLKEKGSLIKLAKVDATVEEELA 90	Db 43 VLVEFYAPWCGHCKALAP-	
	KYFSTLQPGLE	Qy 16 IMCIFYMPTVNSL	
29;	4.1%; Score 169.5; DB 5; Length 482; 22.3%; Pred. No. 0.00099; vative 70; Mismatches 170; Indels 167; Gaps 2	Query Match Best Local Similarity Matches 117; Conser	
	POTENTIAL 54 MW; EA2DE2E		
	00194; THIOREDOXIN; 2. Redox-active center; Signal.	PROSITE, Isomera:	
	; ER_TARGET; UNKNOWN_1.	PROSITE	
	s; TIGRO1130; ER_PDI_fam; 1.	TIGREAM	
	THIOREDOXIN.	PRINTS;	
		DR InterPro; IPR00006	
)886; ER_target.	DR Interpro; IPR00088	
	A80520.1;	DR EMBL; Z22933; CAA80520.1;	
	rasitol. 64:135-144(1994).	RI expression.";	
	ion of the tissues of its	RT Schistosoma manson	
	nz W.;	RA Finken M., Sobek A	
	; PubMed=8078516;	RX MEDLINE=94359529;	
	A	RP SEQUENCE FROM N.A.	
	Schistosomatidae; Schistosoma.	Schistosoma	
	Platyhelminthes:		
	rase homologue precursor.	Protein disulfide	
	MBLrel. 01, Last sequence update) MBLrel. 21, Last annotation update)		
	01, Created)		
	PRELIMINARY; PRT; 482 AA.	Q26593	
		Q26593	
	:: : : : : :	Db 237PLVVEF	
	YERLQKPLLILESDGTVNPQYKKAILTLVKQKYLDSFTP 645	OY 606 SYFRLOKPLLILE	
	LFKKFDEGRADFDGELTR	Db 191 KDAFDHYKIDSKS	
	ASEPALLIARHIEGNIESIPLASIHAQDIVQIIIDALLEMEPEIIVENLE 000	- A A	

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RESULT
Q91Z81
ID Q9
AC Q9
DT 01
DT 01
DT 01
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Q99LF6
ID PLF6
PG Q9
DT 011
DT
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Best Local S
Matches 64
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InterPro; IPRO00065; Thiored.
Pfam; PF00085; Thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
TICREAMS; TICR01136; PG1_dom; 2.
PROSITE; PS00194; THIOREDOXIN; 2.
Q91Z81;
Q91Z81;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99LF6;
Q99LF6;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the
Submitted (FEB-2001) to the
EMBL; BC003285; AAH03285.1;
HSSP; P07237; IMEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; Redox-active center. SEQUENCE 505 AA; 56678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRP58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELTEETFNATVMASDS----IVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINC
                                                                                                                                                                                                                                   NKDLIQGKDLLTAYYDVD----
                                                                                                                                                                                                                                                                                                                                                         LLSTKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVE
                                                                                                                                                                                                                                                                                                                                                                                                                                  E----FKKFISDKDASVVGFFRDLFSDGHSEFLKAASNLRDNYRFAHTNIES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKG---YVITGIYSEEDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANTITCNKYGVSGYPTLKIFRDGEEAGAYDGPRTADGIVS--HLKKQAGPASVPLRTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LELTDENFESRVSDTGSAGLMLVEFFAPWCGHCKRLAPEYEAAATRLKG--IVPLAKVDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LVKEYDDNGEGITIFRPLHLANKFEDKTVAYTEKKMTSGKIKKFIQDSIFGLCPHMTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGKNYNDVVKDKSKDVFVKLYAPWCGHCKALAPVWDELGETFKNSDTVIAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEETFNATV--MASDSIVLFYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADWSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 4.1%; Score 168.5;
Similarity 22.1%; Pred. No. 0.0
64; Conservative 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001 (TrEMBLrel. 17, 2002 (TrEMBLrel. 21, to ER-60 protease.
  (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17,
                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                            LPSYFRLQKPLLILFSDGTVNPQYKKAILTLVKQKYLDS
     19,
19,
21,
  Created)
Last sequence
Last anno
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                YEKNAKGSNYWRNRVMMVAKKFLDA
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3A7CD1C35981C4B3 CRC64;
     sequence update) annotation updat
                                                                                                       505
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cches 125;
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     update)
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Best Local Similarity
""" has 62; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8R6N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8R6N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10029;
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                                                      AA;
     3.9%;
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STRAIN-MB4T / JCM11007;

MEDLINE-21992816; pubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan Genome Res. 12:689-700(2002).

EMBL; AE013214; AAM25873.1; -.

Complete proteome.
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Cricetulus griseus (Chinese hamster).
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lammalla: Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                             Thermoanaerobacter tengcongensis.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanae
NCBI_TaxID-119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ABC-type multidrug/protein/lipid transport system, ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung J.Y., Hwang S.O., Lee G.M.;
"The nucleotide sequence encoding the chinese Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL, AY057063; AAL18160.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO1130; ER_PDI_fam; 1.
TIGREAMS; TIGRO1126; pdi_dom; 2.
PROSITE; PS00194; THIOREDOXIN; UNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000063; Thiored. Pfam; PF00085; thiored; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYDDNGEGITLFRPSHLANKFEDKTVVYTEQKMTSGKIKRFIQESIFGICPHMTEDNKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKYAASLPALLLAR--HTEGKIESIPLASTHAQ----DIVQIITDALLEMFPEITVEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LPSYFRLQKPLLILFSDGTVNPQYKKAILTLVKQKYLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEYLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEEDVLLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADWSDVCTKQNVTEFPIIKMYKKGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LELTDENFESRVSDTGSAGLMLVEFFAPWCGHCKRLAPEYEAAATRLKG--IVPLTKVDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FKKFISDKDASVVGFFRDLFSDGHSEFLKAASNLRD---NYRFAHTNVESLV
                                              66097 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56796 MW; 5F2E38C30794DB76 CRC64
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 166.5; DB 11; Pred. No. 0.0017;
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                              BA6642DF1FBE7545 CRC64;
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and human.";

130;

26;

Gaps

9;

494 78

138

245 609 187

Length Indels

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RESULT
Q91815
ID 805
AC Q5
AC Q6
AC Q6
AC Q6
AC Q6
AC Q7
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                                                                     Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                      O91815 PRELIMINARY;
091815;
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Protein disulfide isomerase
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Last annotation update)
ER-60 (EC 5.3.4.1) (Fragment).
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1; Mismatches 224;
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Matches 61
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VARIANT
NON_TER
                                                                                                                                                                                                                      Submitted (NOV-2000) to the EMB
EMBL; AF325211; AAG45936.1; -.
HSSB; PO7237; IMEX
InterPro; IPR000886; ER_target.
InterPro; IPR000063; Thiored.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9GPH2;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                          PRINTS; PR00421; THIOREDOXIN.
TIGREAMS; TIGR01130; ER_PDI_fam; 1.
TIGREAMS; TIGR01126; pdi_dom; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
                                                                                                                                                                                                      InterPro; IPR000063; Thior Pfam; PF00085; thiored; 2.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. GOO T.W., Yun E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GPH2
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                                                                          PROSITE; PS00014; ER_TARGET; UPROSITE; PS00194; THIOREDOXIN;
                                                                                                                                                                                                                                                                                                                                                              Kwon O.-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mori (Silk moth)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7091;
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                                                  [somerase.
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                                                                                                                                                                                                                                                                                                                                                                                   Hwang J.S.,
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dae; Bombyx.
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HSSP; P07237; 1MEK.
InterPro; IPR000886; ER_target.
InterPro; IPR000863; Thiored.
Pfam; PF00085; thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
TIGREAMS; TIGR01130; ER_PDI_fam; 1.
TIGREAMS; TIGR01126; pdi_dom; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00194; THIOREDOXIN; 2.
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SEQUENCE
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
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MEDLINE-21139750; PubMed-11243858;
Warsame A.A., Vad R., Kristensen T.,
"Characterization of a gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 281:1176-1182(2001). EMBL; AJ302014; CAC33587.1; -.
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156 TIA-EAKEPVI----VQVL------PEDASNLESNTTFYGVAGTLREKFTFVSTKS
                                                                                                                                                                                          435
                                                                                                                                                                                                                                                                                           376 VELTEETFNATVMASDSIVL-FYAGWQAVSMAFLQSYIDVAVKLKGTSTMLLTRINCADW 434
                                                                   494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 KLPLELTV-ELTEETFNATVMASDSIVL-FYAGWQAVSMAFLQSYIDVAVKL-KGTSTML 425
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                                                                YLSGELYKDLILYSSVSVLGLFSPTMKTAKEDFSEAGNYLKGYVITGIYSEE--DVLLLS
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                                                                                                                          KELCQGYEIKGYPTLKVFHGEVEVPSDYQGQRQSQSIVSYMLKQSLPPVSEINATKDLDD
                                                                                                                                                                                    SDVCTKQNVTEFPIIKMYK-KGENPVSYAGMLGTKDLLKFIQLNRISYPVNITSIQEAEE
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                                                                                                                                                                                                                                                                                                                                                                                  ch 3.6%; Score 150.5; DB 3; Length 517; I Similarity 22.5%; Pred. No. 0.025; 79; Conservative 64; Mismatches 161; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Redox-active center. 517 AA; 57788 MW;
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Search completed: March 13, 2003, 17:14:05
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                                                                                                                                                                Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Razusa Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of RECONOMY, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and Biotechnology Center (National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and Biotechnology Center (National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and Biotechnology and Brain Control of the Control o
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Homo sapiens cDNA FLJ40429 fi
AK097748
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NEDO human
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Isogai, T. and Yamamoto, J.
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                                                                                                                                                        annotation: HRI and RAB.
            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TEST12039177"
/tissue_type="testis"
/clone_lib="TEST12"
                                                                                                                                      Location/Qualifiers
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(bases 1 to 161100)

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, J., Birren, B., Linton, L., Nusbaum, C., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Linton, A., Cochepel, Y., Colangelo, M., Collins, S., Colymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Colymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Colymore, A., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Gandgan, J., Gardyna, S., Ginde, S., Goyette, M., Foraham, L., Gandgan, J., Gardyna, S., Ginde, S., Goyette, M., Horton, L., Gandruc, G., Handors, T., Lehoczky, J., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., AAATAGAGAGCATCCCACTAGCTAGCACACATGCACAAGACATAGTTCAAATAATAACAG CARTATTGACACTGGTAAAGCAGAAATACTTGGATTCATTTACTCCATGCTGGTTAAATC TTCCTCTTCTTGTTTTGGTGAATCTGCATTCAGGTGGCCAAGTATTTGCATTTCCTTCAG TTCTAAGTATGATAGATGCCGCAACATCTCAACGTGGCACTAGGAAAGTTCCCCAAGTGTA ACCAGGCTATAATTGAAGAAAACCTTGTATTGTGGCTGAAGAAATTAGAAGCAGGACTAG Eukaryota; Metazoa; Chordata; Cr Mammalia; Eutheria; Primates; Ca 1 (bases 1 to 161100) Birren, B., Linton, L., Nusbaum, C. Homo sapiens, clone RP11-263N17 unordered pieces. AC025659 AC025659.3 GI:8705128 HTG; HTGS_PHASE1; HTGS_DRAFT AC025659 161100 bp Homo sapiens clone RP11-263N17, Homo sapiens Homo sapiens. Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. WORKING and Lander linear HTG DRAFT SEQUENCE, 'n 2729 2747 Karatas, A., 25 15 Allen, N., 2142 2220 2160 2442 2400 2280 2262 2682 2580 2562 2520 2502 2460 2382 2700 2640 2622 JUN-2000 ò

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                                                                                                             The invention relates to an isolated nucleic acid molecule (I) compared a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate can patient;
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) selecting a composition for inhibiting prostate cancer in a patient;
) assessing the prostate cell carcinogenic potential of a compound;
) determining whether prostate cancer has metastasized in a patient;
)) assessing the aggressiveness or indolence of prostate cancer in a
is also useful
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